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MOAT-B
MRP 1 MALRGFCSADGSDPLWDMVNTWNTSNPDFTKCFONTVLVWPCFYWACFPFYFLYLSRHRDGYIQMTPLNKTALGFLWVCHADLFYSFWERSGI 100

MOAT-B 1MLP 3

MRP 101 FLAPVFLVSPITLLGITTLLATFLIQLERRKGVQSSGIMTLFWLVALCALAILRSKINTALKEDAQVDLFRDITFYVYFSLLLIQLVLSCFSDRSPLFSE 200

MOAT-B 4 VYQEVKPNPLQDANICSRVFFWMLNPLFKIGHKRRLEEDHYSVLPEDRSQHLGEELQGFWDKEVLRAENDAOK 77

MRP 201 TIHDPNPCPESSASFLSRITFWMITGLIVRGYRQPLEGSDLSLNKEDTSEQVVPVLVKNWKKCAKTRKQPKVYVSSKDPAPQKSSKVDANEVEAL 300

MOAT-B 78PSLTRAIIKCYWKSIVLVGIFTLIESAKVIOPIFLGKIINYFENYDPMDSVALNTAYAYATVLTFTCLILAILHHLYFYHVQCAGMRL 166

MRP 301 IVKSPQKEWNPFLFKVLYKTGPGYFLMSFFFAIHDLMHMFSGPQILKLLIKFVNDTKAPDWQGYFYTLLFVTACQLTLVLHQYFHCIFVSGMRI 395

MOAT-B 167 RVAMCHMIYRKALRLSNMAMGKTTTQCIQVNLNSNDVNKFDQVTVFLHFLWAGPLQAIATALLWMEIGISCLAGHAVLIILLPLQSCFGKLFSSLSRKTA 266

MRP 396 KTAIVGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFDLATYINMIWSAPLOVILALYLLWNLGPSVLAVVAVMLHVPNAVMAHMKTKTYQVAHM 495

MOAT-B 267 TFTDARIRTHNEVITGIRIIMYAWKSFNSLITNLRKKEISKILRSSCLRMNLASFSSASKIIVFVTFTTYVLLG...SVITASRVFVAVTLYGAVRLT 364

MRP 496 KSKDNRIKLMNEILNGIKVLKLYAWELAFKDKVLAIROEELKVLKKSAYLSAVGTFTWCTPFLVALCTFAVYVITIDENILDAQTAFVSLALFNILRFP 595

MOAT-B 365 VTLFFPSAIERVSEAIVSIRRIOTFLLLDEIS...ORNRLPSDGKKMHHVQDPTAFWDKASETPTLQGLSFTVRPGELLAVVGPVGACKSSLLSAVLG 460

MRP 596 LNI.LPMVISSIVQASVSLKRLRIFLSHEELEPDSIERRPVKGGGTNSITVRNATFTWAR.SDPPTLNGITFSIPEGALVAVVGQVCGCKLSLLSALLA 693

MOAT-B 461 ELAPSHGLVSVHGRIAYVSQPPWVFSCTLSRNSILFGKKYKERYEKVICALKDKDLQLEDGLTVIGDRGTTLSGGQKARVNLARAVYQDADIYLLDD 560

MRP 694 EMDKVEGHVAIKGSVAYVPOQAWIQNDSLRNIFLGCQLEEPYRSVIOACALLPDLEILPSGDRTEICEKGVNLSCGQKQVSLARAVYSNADIYLFDD 793

MOAT-B 561 PLSAVDAEVSRLHFLCICQ...ILHEKITLVTHQLQYLKAASQILILKDGKMKVQKGTYTEFLKSGIDFGSLK...KDNEESEOPVPG... 645

MRP 794 PLSAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMYLPQVDVIVMSGKISEMGSYQELLARDGAFAEFLRTYASTEQEQAENGVTGVSQPGKEA 893

MOAT-B 646TPTLRNRTFSESSVWSQSSRPSLKDGALESQDT...ENVPTLSEENRSEKGVGQAYKYFRAGAHWIVFIFLILLNTAAQVAVYVLO 731

MRP 894 KOMENGMLVTDGACKQLQRLSSSSYSQDISRHHNSTAELQKAEAKKEETWKLHEADKAQTCQVKLSVYWDYHKAIGLIFISFLSIFL.MCNHVSALAS 992

MOAT-B 732 DWLWLYWANKQSHLNVTVNGGNNVTEKLDLWNLGCIYSGTLVATVLFGIARSLLVFVVLVNSSQTLHNKMFESILKAPVLFDRNPGRILNRFSKDIGH 831

MRP 993 NYWLSLWTD...DPIVNGTQEHKVR...LSVYGALGISQGIADVFSMAVSIIGGILASRCLHVDLLHSILRSPHSFFERTPSGNLVRFSKELDT 1082

MOAT-B 832 LDDLPLTFLDFIQTLLQVGVVSVAVAPIWIAIPLVPLGIIIFIPLRRYFLETSRDVKRLESTTRSPVFSHLSSSLQGLWITIRAYKAEERCQELFDAHQ 931

MRP 1083 VDSMIPEVIKMFGLFNVIGACIVILLATPIAAIIPPLGLIYFFVQRFYVASSRQLKRESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLV 1182

MOAT-B 932 DLHSEAWFLFTLTSRWFVRLDAICAMFVIIAFAVGLSLILAKTLDAQVGLALSVALTLMGHFOWCVROSAEVENMMISVERVIEYTDLEKEAPWEYOK.R 1030

MRP 1183 DENOKAYPSIVANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVYSIQVTTYLNWLVMSSEMETNIVAVERLKEYSETEKEAPWQIQETR 1282

MOAT-B 1031 PPPAWPHEGVIIIFDNVNFHSPGGLVVLKHLTALIKSOEKGIVGRTGAGKSSLSALFRSE.PEGKIWDKILTTEIGLHDLRKMSIIPQEPVLTG 1129

MRP 1283 PPSWNPQVGRVEFRNYCLRYREDLDFVLRHINVTINGGEKVGIVGRTGAGKSSLTGLFRINESAECEIIDGINIAKIGLHDLRFKITIIPQDPVLFSG 1382

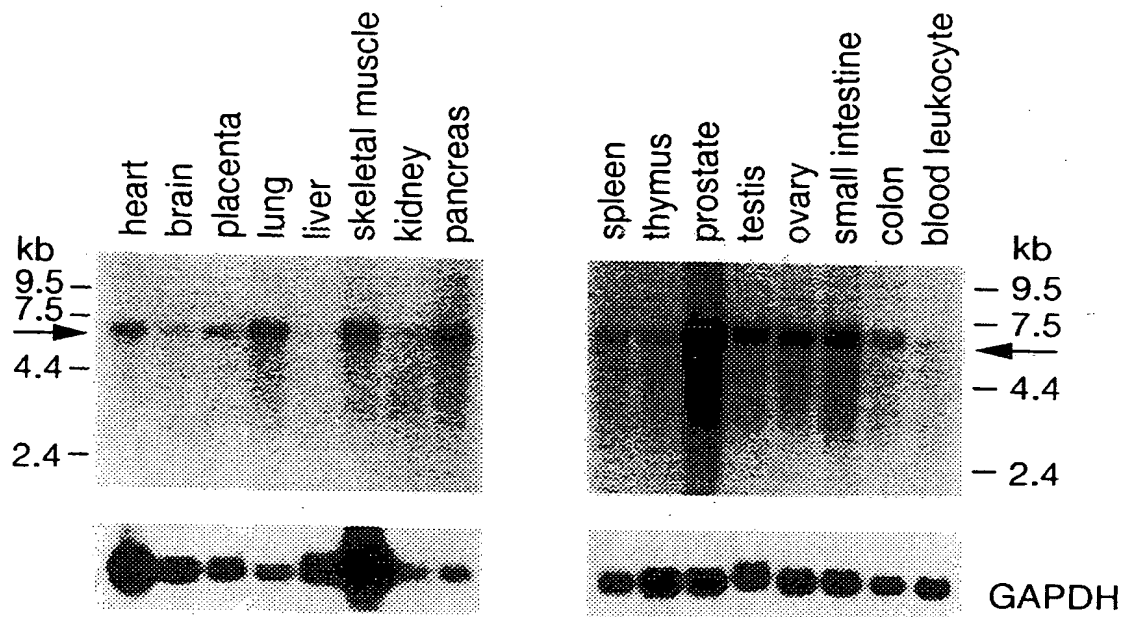
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MRP 1383 SLRNKLDPPSQYSDEEVNTSLELAHLKDFVSALPDKLDHECAEGENLSVGQRQLVCLARALLRKTKILVLEATAVDETDDLIOSTIRTQFEDCTVL 1482

MOAT-B 1230 TIAHRLNTIIDSCKIMVLDGRLKEYDEPYVLLQNKESLFYKMWQQLKAEAAALTETAKQVYFKRNYHIGHTDMVNTNSNGOPSTLTIFETAL 1325

MRP 1483 TIAHRLNTIMDYTRVIVLDKGEIOEYGA PSDLQOR.GLFYSMAKDAGLV 1531

Figure 1

**Figure 3**

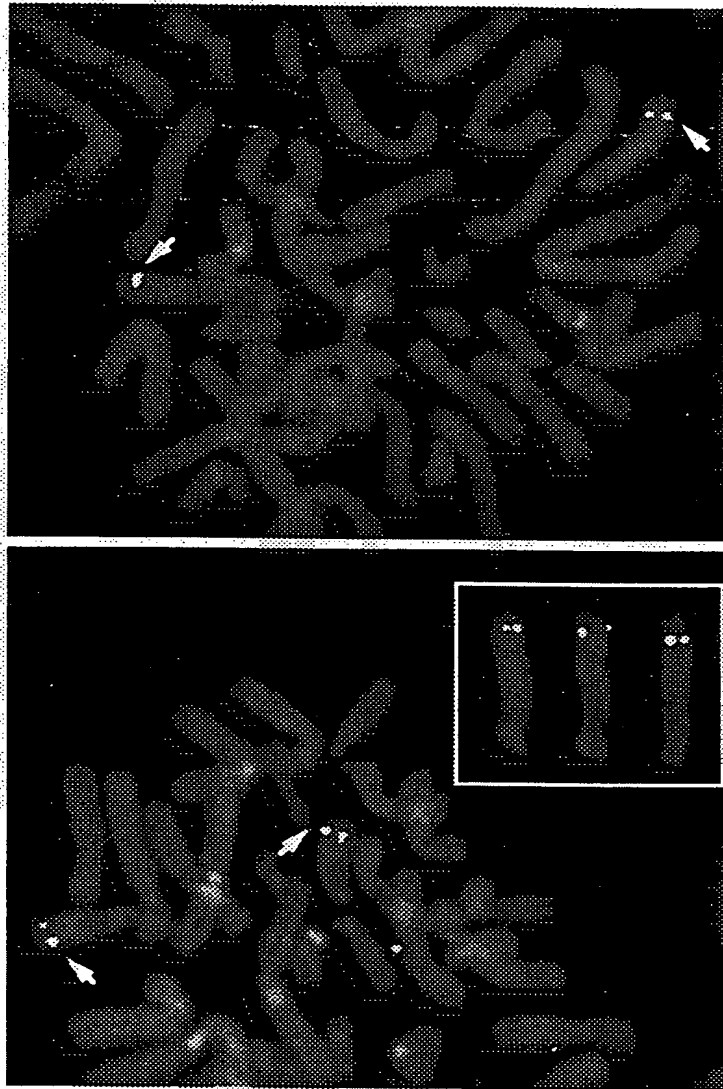


Figure 4

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Fig. 5A

1 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRR TRPLECQDAL ETAARAEGLS
 61 LDASMHSQLR ILDEEHPK GK YHHGLSALKP IRTTSKHQHP VDNAGLFSM TFSWLSSLAR
 121 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTL
 181 TM1 LSIVCLMITQ LAGFSGPAPM VKHLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW
 241 TM2 ALNYRTGVRL RGAILTMAFK KILKLNKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG
 301 TM3 PVVAILGMIY NVIILGPTGF LGSVAVFILFY PAMMFASRLT AYFRRKCVAA TDERVQKMNE
 361 TM4 VLTYYKFIKM YAWVKAFSOS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV
 421 TM5 HMTLGFDLTA AQFTVVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK
 481 NKPASPHIKI EMKNATLAWD SSHSSIONSP KLTPEKMKDK RASRGKKEKV RQLQRTEHQA
 541 TM6 VLAEQKGHLL LDSERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVSGG
 601 NBF1 A KTSILISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILPGKEYD EERYNSVLNS
 661 CCLRPDLAIL PSSDLTEIGE RGANLGGQR ORISLARALY SDRSIYILDD PLSALDAHV
 721 NBF1 C B NHIFNSAIRK HLKSKTVLFV THQLQYLVD C DEVIFMKEGC ITERGTHEEL MNLNGDYATI
 781 FNNLLLGETP PVEINSKKE T SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VOLEEKQOGS
 841 TM7 VPWSVYGVYI QAAGGPLAF L VIMALFHLNV GSTAFSTWWL SYWIKQSGN TTVTRGNETS
 901 TM8 VSDSMKDNPH MQYYASIIAL SMAVMLILKA IRGVVFKGT LRASSRLHDE LFRRILRSPM
 961 TM9 KFFDTTPTGR ILNRFSKDM D EVDVRLPFA EMFIONVILV FFCVGMIAGV FPWFLVAVGP
 1021 TM10 LVILFVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL
 1081 TM11 LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISTAVOLT
 1141 TM12 GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM
 1201 NBF2 RYRENPLVL KVSFTIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRISD
 1261 IGLADLRSLK SIIPQEPVLF SGTVRNLD PNOYTEDQIW DALERTHME CIAQLPLKLE
 1321 SEVMENGDNF SVGEROLL CI ARALLRECKI LILDEATAAM DTETDLIQE TIREAFADCT
 1381 C B MLTIAHRLHT VLGS DRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG

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Fig. 5B

1 MGPMDALCGS GELGSKFWDS NLSVHTENPD LTPCFQNSLL AWVPCIYLVV ALPCYLLYLK TM1
 61 HHCRGYIILS HLSKLMVLG VLLWCVSWAD LFYSFHGLVH GRAPAPVFFV TPLVVGVTML TM2
 121 LATLLIQYER LOGVSSGVL IIFWFLCVVC AIVPFRSKIL LAKAEGEISD PFRFTTFYIH TM3
 181 FALVLSALIL ACFREKPPFF SAKNVDPNPY PETSUGFLSR LFFWWFTKMA IYGYRHPLEE TM4
 241 KDLWSLKEED RSQMVVQQLL EAWRKQEKQT ARHKASAAPG KNASGEDEV L GARPRPRKP TM5
 301 SFLKALLATF GSSFLISACF KLIQDILLSFI NPQLLSILIR FISNPMAPSW WGFLVAGLMF TM6
 361 LCSMMQSLIL QHYHYIFVT GVKFRTGIMG VIYRKALVIT NSVKRASTVG EIVNLSMVDA TM7
 421 ORFMDLAPFL NLLWSAPLOI ILATYFLWQN LGPSVLAGVA FMVLLIPLNG AVAVKMRAPQ TM8
 481 VKQMKLDSR IKLMSEILNG IKVLKLYAWE PSFLKQVEGI RQELQLLRT AAYLHTTTTF TM9
 541 TWMCSPLVLT LITLWVYVYV DPNNVLD AEFVSVSLFNI LRLPLNMLPQ LISNLTQASV TM10
 601 SLKRIQQFLS QEELDPOSVE RKTISPGYAI TIHSGTFTWA QDLPTLHSL DIQVPGKALY NBF1
 661 AVVGPVCGCK SSLVSALLGE MEKLEGKVHM KGSVAIVPQO AWIONCTLQE NVLFGKALNP A
 721 KRYQOTLEAC ALLADLEMLP GGDQTEIGEK GINLSGGORQ RVSLARAVYS DADIFLLDDP NBF1
 781 LSAVDSEVAK HIFDEHIGPE GVLAKTRVL VTHGISFLPQ TDFIIVLADG QVSEMGYPYA B
 841 LLQRNGSFAN FLCNYAPDED QGHLEDSWTA LEGAEDKEAL LIEDTLSNHT DLTDNDPVTY C
 901 VVQKQFMRQL SALSSDGEQ GRPVPRRLG PSEKQVTEA KADGALTQEE KAAIGTVELS
 961 VFWDYAKAVG LCTTLAICLL YVGOSAAAIG ANVWLSAWTN DAMADSRQNN TSLRLGVYAA TM12
 1021 LGILQGFVLH LAAMAHAGG IQAARVLEQA LLENKIRSPQ SFFDTTPSGR ILNCFSKDIY TM13
 1081 VVDEVLPVI LMLLNSFFNA ISTLVVIMAS TPLFTTVILP LAVLYTLVQR FYAATSRQLK TM14
 1141 RLESVSRSPI YSHFSETVTG ASVIRAYNRS RDEFIISDTK VDAQRSCYP YIISNRWLSI TM15
 1201 GVEFVGNCVV LFAALFAVIG RSSLNPLGVG LSVSYSLQVT FALNWHIRM SDLESNIVAV TM16
 1261 ERVKEYSKTE TEAPWVVEGS RPPEGWPPRG EVEFRNYSVR YRPGDLVLRL DLSLEHVHGE NBF2
 1321 KVGIVGRTGA GKSSMTLCLE RILEAAKGEI RIDGLNVADI GLHDLRSOLT IIPQDPILFS A
 1381 GTLRMNLDPF GSYSEEDIWW ALELSHLHTF VSSQAGLDF QCSEGGENLS VGQRQLVCLA NBF2
 1441 RALLRKSRL VLDEATAAID LETDNLIQAT IRTQFDTCTV LTIAHRLNTI MDYTRVLVLD C
 1501 KGVVAEFDSP ANLIAARGIF YGMARDAGLA B

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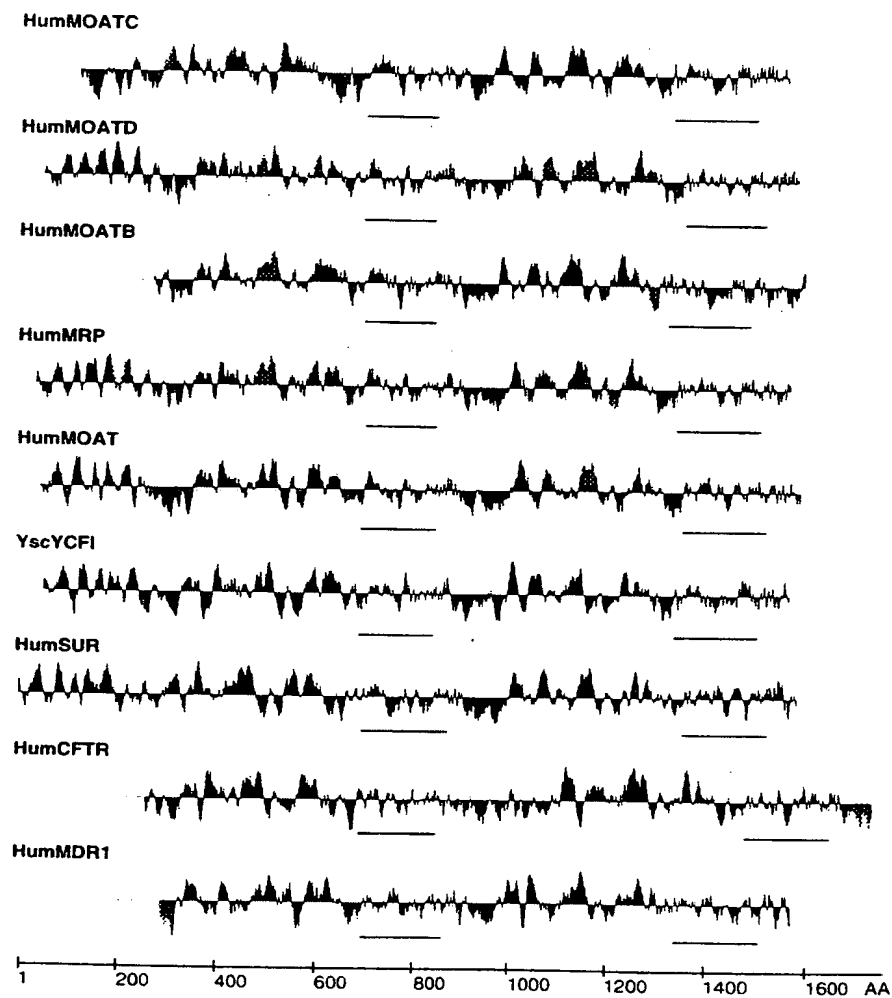


Fig. 6B

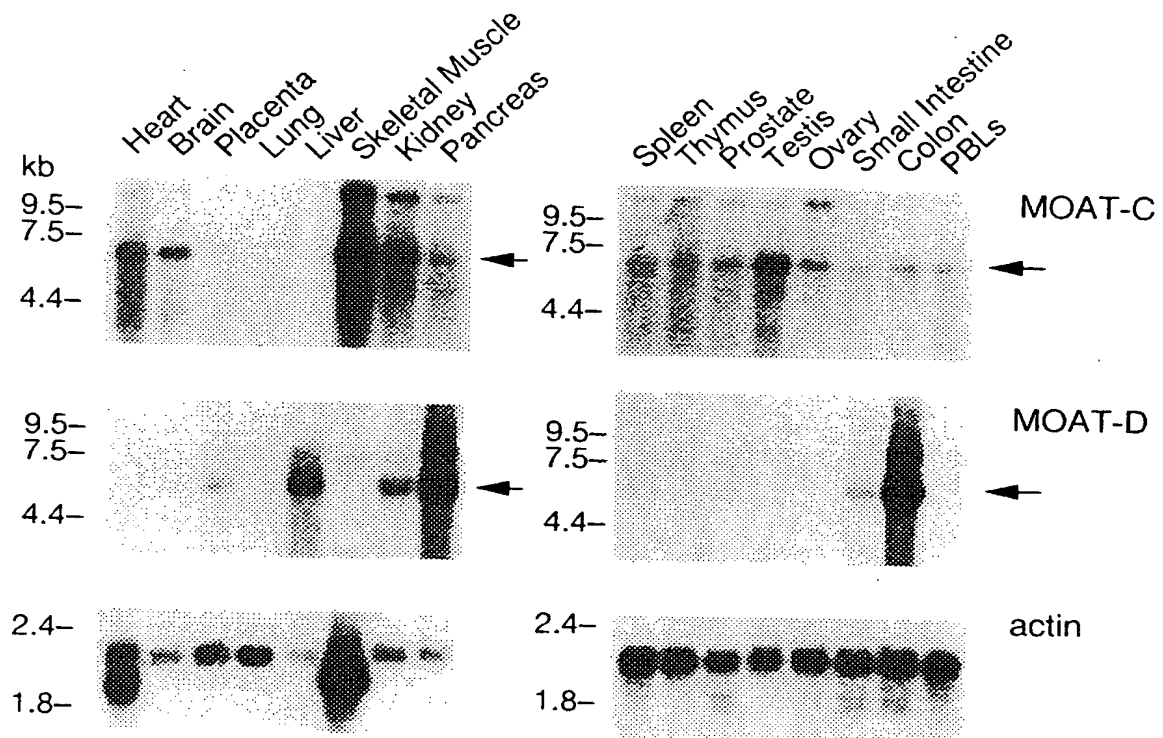
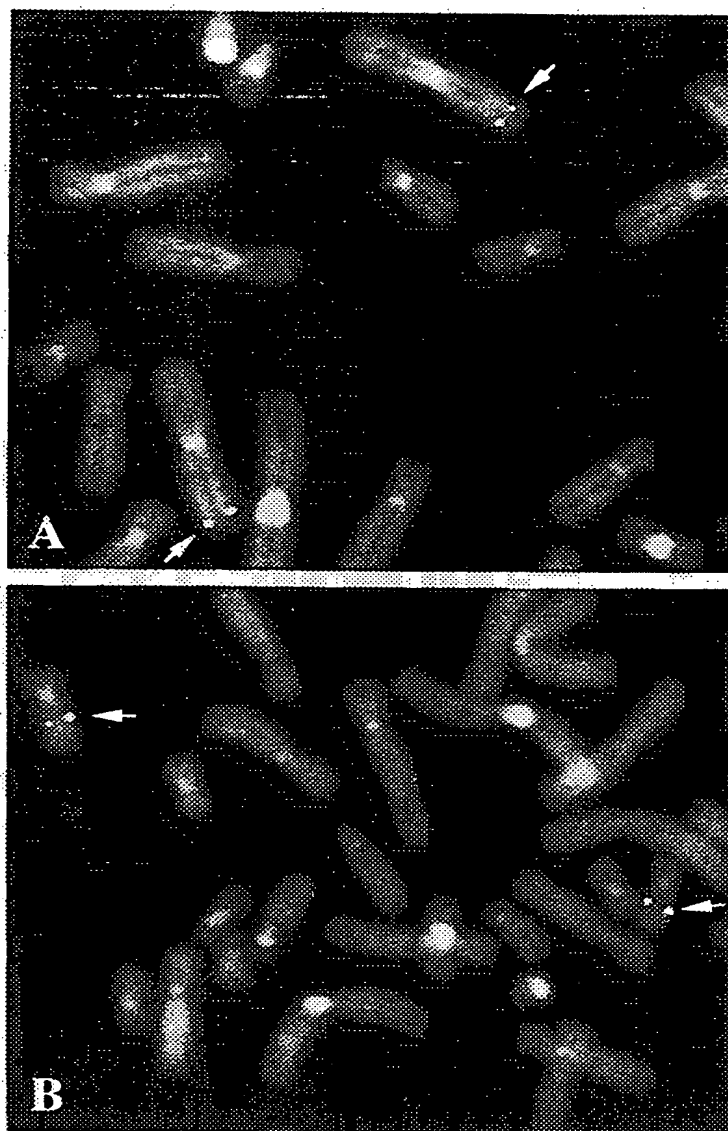


Figure 7

**Figure 8**

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1 MAAPAEPCAG QGVW[•]NOTEPE PAATSLLSLC FLRTAGVWVP PHYLWVLGPI YLLFIHHHGR
 61 GYLMSPLFK AKMVLGFALI VLCTSSVAVA LWKIQOQTPE APEFLIHPTV WLTMTSFAVF
 121 LIHTEKKGKV QSSGVLFQYW LLCFVLPATN AAQOASGAGF QSDPVRHLST YLCLSLVVAQ
 181 FVLSCLADQP PFFPEDPQOS NPCPETGAAF PSKATFWWVS GLVWRGYRRP LRPKDLWSLG
 241 RENSSEELVS RLEKEWMRNR SAARRHNKAI AFKRKGGSGM KAPETEPFLR QEGSQWRPLL
 301 KAIWQVFHST FLLGTLSLII SDVFRFTVPK LLSLFLEFIG DPKPPAWKGY LLAVLMFLSA
 361 CLQTLFEQQN MYRLKVPQMR LRSAITGLVY RKVLALSSGS RKASAVGDV VNLVSDVQRL
 421 TESVLYLNGL WLPLVWIVVC FVYLWQLLGP SALTAIAVFL SLLPLNFFIS KKRHHHQBEO
 481 MRQKDSRRL TSSILRNSKT IKPHGWEGAF LDRVLGIRGQ ELGALRTSGL LFSVSLVSFO
 541 VSTFLVALV FAVHTLVAEN AMNAEKAFVT LTVLNILNKA QAFLPFSIHS LVQARVSFDR
 601 LVTFLCLEEV DPGVVDSSSS GSAAGKDCIT IHSATFAWSQ ^{→ NBF1}ESPPCLHRIN LTVPOGCLLA
 661 VVGPVGAGKS SLLSALLGEL SKVEGFVSIE GAVAYVPQEA WVQNTSVVEN VCFGQELDPP
 721 ^AWLERVLEACA LQPDVDSFPE GIHTSIGEQG MNLSSGQKOR LSLARAVYRK AAVYLLDDPL
 781 ^{NBF1←}AALDAHVGQH VFNQVIGPGG LLQGTTRILV ^CTHALHILPOA DWIIVLANGA ^BIAEMGSYQEL
 841 LQRKGALVCL LDQARQPGDR GEGETEPGTS TKDPRGTSAG RRPRLRRERS IKSVPKDRRT
 901 TSEAQTEVPL DDPDRAGWPA GKDSIQYGRV KATVHLAYLR AVGTPLCLYA LFLFLCQOVA
 961 SFCRGYWLSL WADDPVAVGGQ QTQAALRGGI FGLLGCLQAI GLFASMAAVL LGGARASRL
 1021 FORLLWDVVR SPISFFERTP IGHLLNRFSK ETDVTDVDIP DKLRSLMYA FGLLEVSLV
 1081 AVATPLATVA ILPLFLLYAG FQSLYVSSC QLRRLESASY SSVCSHMAET FQGSTVVRAF
 1141 RTOAPFVAQN NARVDESQRI SFPRLVADRW LAANVELLGN GLVFAAATCA VLSKAHLSAG
 1201 LVGFSVSAAL QVTQALQWV RNWTDLENSI VSVERMODYA WTPKEAPWRL PTCAAQPPWP
 1261 QGGQIEFRDF GLRYRPELPL ^{→ NBF2}AVQGVSLKIH AGEKVGIVGR TGAGKSSLAS GLLRLQEAEE
 1321 GGIWIDGVPI AHVGLHTLRS RISIIPQDPI LFPGLRMNL ^ADLLQEHSDEA IWALETVQL
 1381 KALVASLPGQ LOYKCADRGE DLSVGQKQLL CLARALLRKT QILILDEATA ^{NBF2←}AVDPGTELOM
 1441 ^CQAMLGSWFAQ CTVLLIAHRL ^BRSVMDCARVL VMDKGQVAES GSPAQLLAQK GLFYRLAQES
 1501 GLV

Figure 9

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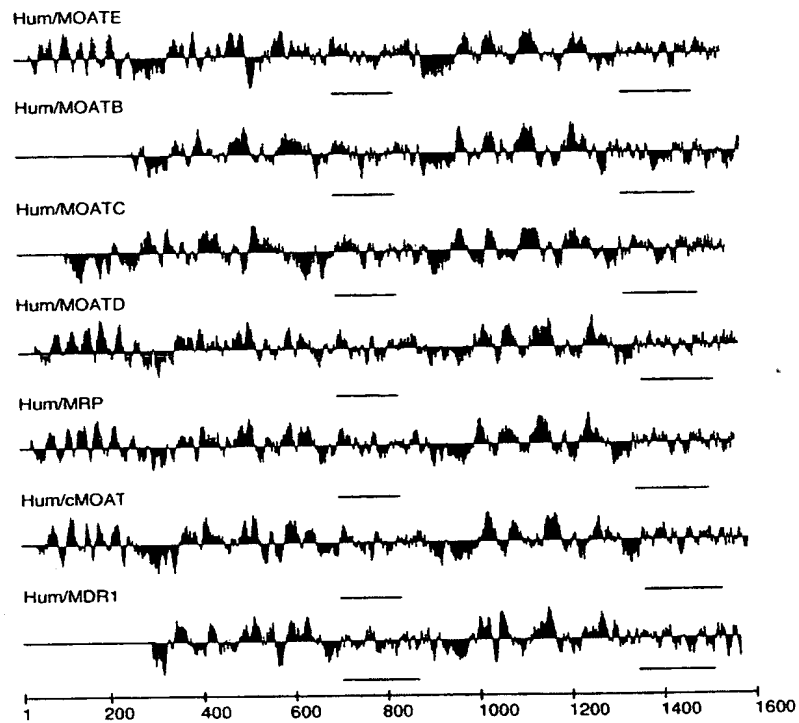


Figure 10

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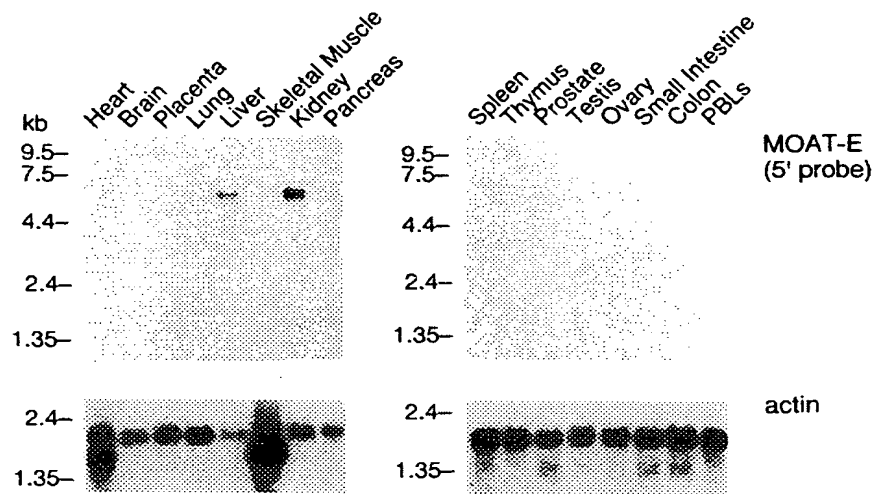


Figure 11

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MOAT B cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA
 1 -----+-----+-----+-----+-----+-----+ 60
 TACGACGGGCACATGGTCTCCACTTCGGGTTGGGCGACGTCCTGCGCTTGTAGACGAGT
 a M L P V Y Q E V K P N P L G D A N I C S -

CGCGTGTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG
 61 -----+-----+-----+-----+-----+-----+ 120
 GCGCACAAGAAGACCACCGAGTTAGGGAACAAATTTTAACCGGTATTTGCCTCTAATCTC
 a R V F F W W L N P L F K I G H K R R L E -

GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG
 121 -----+-----+-----+-----+-----+-----+ 180
 CTTCTACTATACATAAGTCACGACGGTCTTCTGGCGAGTGTCGTGGAACCTCTCCTCAAC
 a E D D M Y S V L P E D R S Q H L G E E L -

CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA
 181 -----+-----+-----+-----+-----+-----+ 240
 GTTCCCAAGACCCTATTTCTTCAAAATTCTCGACTCTTACTGCGTGTCTTCGGAAGAAAT
 a Q G F W D K E V L R A E N D A Q K P S L -

ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTACGTTA
 241 -----+-----+-----+-----+-----+-----+ 300
 TGTCTCGTTAGTATTTACAATGACCTTTAGAATAAATCAAAACCCTTAAAAATGCAAT
 a T R A I I K C Y W K S Y L V L G I F T L -

ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT
 301 -----+-----+-----+-----+-----+-----+ 360
 TAACTCCTTTACGGTTTCATTAGGTCGGGTATAAAAACCCTTTTAAATAATTAATAAAA
 a I E E S A K V I Q P I F L G K I I N Y F -

GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG

Figure 12A

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361 -----+-----+-----+-----+-----+ 420
CTTTTAATACTAGGGTACCTAAGACACCGAAACTTGTGTCGCATGCGGATACGGTGCCAC

a E N Y D P M D S V A L N T A Y A Y A T V -

CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTATCACGTTTCAG

421 -----+-----+-----+-----+-----+ 480
GACTGAAAAACGTGCGAGTAAAACCGATATGACGTAGTGAATATAAAAAATAGTGCAAGTC

a L T F C T L I L A I L H H L Y F Y H V Q -

TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT

481 -----+-----+-----+-----+-----+ 540
ACACGACCCTACTCCAATGCTCATCGGTACACGGTATACTAAATAGCCTTCCGTGAAGCA

a C A G M R L R V A M C H M I Y R K A L R -

CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT

541 -----+-----+-----+-----+-----+ 600
GAATCATTGTACCGGTACCCCTTCTGTTGGTGTCCGGTCTATCAGTTAGACGACAGGTTA

a L S N M A M G K T T T G Q I V N L L S N -

GATGTGAACAAGTTTGATCAGGTGACAGTGTTCCTTACACTTCCTGTGGGCAGGACCACTG

601 -----+-----+-----+-----+-----+ 660
CTACACTTGTTCAAAGTAGTCCACTGTCAAGAATGTGAAGGACACCCGTCCTGGTGAC

a D V N K F D Q V T V F L H F L W A G P L -

CAGGCGATCGCAGTGAAGTGCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG

661 -----+-----+-----+-----+-----+ 720
GTCCGCTAGCGTCACTGACGGGATGAGACCTACCTCTATCCTTATAGCACGGAACGACCC

a Q A I A V T A L L W M E I G I S C L A G -

ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA

721 -----+-----+-----+-----+-----+ 780
TACCGTCAAGATTAGTAAGAGGACGGGAACGTTTCGACAAAACCCTTCAACAAGAGTAGT

a M A V L I I L L P L Q S C F G K L F S S -

CTGAGGAGTAAAACTGCAACTTTACGGATGCCAGGATCAGGACCATGAATGAAGTTATA

781 -----+-----+-----+-----+-----+ 840

Figure 12B

SUBSTITUTE SHEET (RULE 26)

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GACTCCTCATTTTGACGTTGAAAGTGCCTACGGTCCTAGTCCTGGTACTTACTTCAATAT
 a L R S K T A T F T D A R I R T M N E V I -
 ACTGGTATAAGGATAATAAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC
 841 ----- + ----- + ----- + ----- + ----- + 900
 TGACCATATTCTATTATTTTACATGCGGACCCTTTTCAGTAAAAGTTTAGAATAATGG
 a T G I R I I K M Y A W E K S F S N L I T -
 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT
 901 ----- + ----- + ----- + ----- + ----- + 960
 TAAACTCTTCTTCTCTAAAGGTTCTAAGACTCTTCAAGGACGGAGTCCCCCTACTTA
 a N L R K K E I S K I L R S S C L R G M N -
 TTGGCTTCGTTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG
 961 ----- + ----- + ----- + ----- + ----- + 1020
 AACCGAAGCAAAAAGTCACGTTTCGTTTTAGTAGCACAAACACTGGAAGTGGTGGATGCAC
 a L A S F F S A S K I I V F V T F T T Y V -
 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTTCGTGGCAGTGACGCTGTATGGGGCT
 1021 ----- + ----- + ----- + ----- + ----- + 1080
 GAGGAGCCGTCACACTAGTGTGCGTTCGGCGCACAAAGCACCGTCACTGCGACATACCCCGA
 a L L G S V I T A S R V F V A V T L Y G A -
 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC
 1081 ----- + ----- + ----- + ----- + ----- + 1140
 CACGCCGACTGCCAATGGGAGAAGAAGGGGAGTCGGTAACTCTCCCACAGTCTCCGTTAG
 a V R L T V T L F F P S A I E R V S E A I -
 GTCAGCATCCGAAGAATCCAGACCTTTTGTCTACTTGATGAGATATCACAGCGCAACCGT
 1141 ----- + ----- + ----- + ----- + ----- + 1200
 CAGTCGTAGGCTTCTTAGGTCTGGAAAAACGATGAACTACTCTATAGTGTGCGGTTGGCA
 a V S I R R I O T F L L L D E I S O R N R -
 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT
 1201 ----- + ----- + ----- + ----- + ----- + 1260
 GTCGACGGCAGTCTACCATTTTCTACCACGTACACGTCCTAAAATGACGAAAAACCCTA

Figure 12C

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PCT/US99/06644

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a Q L P S D G K K M V H V Q D F T A F W D .
AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG
1261 ----- + ----- + ----- + ----- + ----- + ----- + 1320
TTCCGTAGTCTCTGGGGTTGAGATGTTCCGGAAAGGAAATGACAGTCTGGACCGCTTAAC

a K A S E T P T L Q G L S F T V R P G E L .
TTAGCTGTGGTTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG
1321 ----- + ----- + ----- + ----- + ----- + ----- + 1380
AATCGACACCAGCCGGGGCACCCTCGTCCCTTCAGTAGTGACAATTCACGGCACGAGCCC

a L A V V G P V G A G K S S L L S A V L G .
GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG
1381 ----- + ----- + ----- + ----- + ----- + ----- + 1440
CTTAACCGGGGTTCAAGTGCACGACAGTGCACGTACCTTCTTAACGGATACACAGAGTC

a E L A P S H G L V S V H G R I A Y V S Q .
CAGCCCTGGGTGTTCTCGGGAAGTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA
1441 ----- + ----- + ----- + ----- + ----- + ----- + 1500
GTCCGGACCCACAAGAGCCCTTGAGACTCCTCATTATAAAATAAACCTTCTTTATACTT

a Q P W V F S G T L R S N I L F G K K Y E .
AAGGAACGATATGAAAAAGTCATAAAGGCTTGCTGCTCTGAAAAAGGATTTACAGCTGTTG
1501 ----- + ----- + ----- + ----- + ----- + ----- + 1560
TTCCTTGCTATACTTTTTTCAGTATTTCCGAACACGAGACTTTTTCCTAAATGTCGACAAC

a K E R Y E K V I K A C A L K K D L Q L L .
GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACACGCTGAGTGGAGGGCAGAAA
1561 ----- + ----- + ----- + ----- + ----- + ----- + 1620
CTCCTACCACTAGACTGACACTATCCTCTAGCCCCTTGGTGCGACTCACCTCCCGTCTTT

a E D G D L T V I G D R G T T L S G G Q K .
GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT
1621 ----- + ----- + ----- + ----- + ----- + ----- + 1680
CGTGCCCATTTGGAACGTTCTCGTCACATAGTTCTACGACTGTAGATAGAGGACCTGCTA

Figure 12D

18/56

a A R V N L A R A V Y Q D A D I Y L L D D -
CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTTGAAGTGTGTATTTGTCAA
1681 -----+-----+-----+-----+-----+-----+ 1740
GGAGAGTCACGTCATCTACGCCTTCAATCGTCTGTGAACAAGCTTGACACATAAACAGTT

a P L S A V D A E V S R H L F E L C I C O -
ATTTTGCATGAGAAGATCACAAATTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA
1741 -----+-----+-----+-----+-----+-----+ 1800
TAAAACGTACTCTTCTAGTGTTAAATCACTGAGTAGTCAACGTCATGGAGTTTCGACGT

a I L H E K I T I L V T H Q L Q Y L K A A -
AGTCAGATTCTGATATTGAAAGATGGTAAATGGTGCAGAAGGGGACTTACACTGAGTTC
1801 -----+-----+-----+-----+-----+-----+ 1860
TCAGTCTAAGACTATAACTTTCTACCATTTTACCACGTCTCCCCTGAATGTGACTCAAG

a S Q I L I L K D G K M V Q K G T Y T E F -
CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA
1861 -----+-----+-----+-----+-----+-----+ 1920
GATTTTAGACCATATCTAAAACCGAGGGAAAATTTCTTCTATTACTCCTTTCACTTGTT

a L K S G I D F G S L L K K D N E E S E Q -
CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG
1921 -----+-----+-----+-----+-----+-----+ 1980
GGAGGTCAAGGTCCTTGAGGGTGTGATTCCTTAGCATGGAAGAGTCTCAGAAGCCAAACC

a P P V P G T P T L R N R T F S E S S V W -
TCTCAACAATCTTCTAGACCTCCTTGAAAGATGGTGTCTCTGGAGAGCCAAGATACAGAG
1981 -----+-----+-----+-----+-----+-----+ 2040
AGAGTTGTTAGAAGATCTGGGAGGAACTTTCTACCACGAGACCTCTCGGTTCTATGTCTC

a S Q Q S S R P S L K D G A L E S Q D T E -
AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTTCAGGCC
2041 -----+-----+-----+-----+-----+-----+ 2100
TTACAGGGTCAATGTGATAGTCTCCTCTTGGAAGACTTCTTTTCAACCAAAAGTCCGG

a N V P V T L S E E N R S E G K V G F Q A

Figure 12E

SUBSTITUTE SHEET (RULE 26)

WO 99/49735

PCT/US99/06644

19/56

TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA
2101 -----+-----+-----+-----+-----+-----+ 2160
ATATTCTTAATGAAGTCTCGACCACGAGTGACCTAACAGAAGTAAAAGGAATAAGAGGAT

a Y K N Y F R A G A H W I V F I F L I L L -

AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC
2161 -----+-----+-----+-----+-----+-----+ 2220
TTGTGACGTGAGTCCAACGGATACACGAAGTTCTAACCACCGAAAGTATGACCCGTTTG

a N T A A Q V A Y V L Q D W W L S Y W A N -

AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT
2221 -----+-----+-----+-----+-----+-----+ 2280
TTTGTTCATACGATTTACAGTGACATTTACCTCCTCCTTTACATTGGCTCTTCGATCTA

a K Q S M L N V T V N G G G N V T E K L D -

CTTAAGTGGTACTTAGGAATTTATTACAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA
2281 -----+-----+-----+-----+-----+-----+ 2340
GAATTGACCATGAATCCTTAAATAAGTCCAAATTGACATCGATGGCAAGAAAAACCGTAT

a L N W Y L G I Y S G L T V A T V L F G I -

GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAACTTTGCACAACAAA
2341 -----+-----+-----+-----+-----+-----+ 2400
CGTTCTAGAGATAACCATAAGATGCAGGAACAATTGAGAAGTGTTTGAAACGTGTTGTTT

a A R S L L V F Y V L V N S S Q T L H N K -

ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA
2401 -----+-----+-----+-----+-----+-----+ 2460
TACAAACTCAGTTAAGACTTTCGAGGCCATAATAAGAACTATCTTTAGGTTATCCTTCT

a M F E S I L K A P V L F F D R N P I G R -

ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTGCTGCCGCTGACGTTT
2461 -----+-----+-----+-----+-----+-----+ 2520
TAAATTTAGCAAAGAGGTTTCTGTAACCTGTGAACCTACTAAACGACGGCGACTGCAAA

a I L N R F S K D I G H L D D L L P L T F

Figure 12F

20/56

TTAGATTTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG
2521 -----+-----+-----+-----+-----+-----+ 2580
AATCTAAAGTAGGTCTGTAACGATGTTACCAACCAACCAGAGACACCGACACCGGCAC

a L D F I Q T L L Q V V G V V S V A V A V -

ATTCTTGGATCGCAATACCCTTGGTTCCCTTGAATCATTTTCATTTTCTTCGGCGA
2581 -----+-----+-----+-----+-----+-----+ 2640
TAAGGAACCTAGCGTTATGGGAACCAAGGGGAACCTTAGTAAAAGTAAAAAGAAGCCGCT

a I P W I A I P I V P L G I I F I F L R R -

TATTTTTTGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACCTCGGAGTCCAGTG
2641 -----+-----+-----+-----+-----+-----+ 2700
ATAAAAAACCTTTCAGTTCTCTACACTTCGCGGACCTTAGATGTTGAGCCTCAGGTCAC

a Y F L E T S R D V K R L E S T T R S P V -

TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA
2701 -----+-----+-----+-----+-----+-----+ 2760
AAAAGGGTGAACAGTAGAAGAGAGGTCCCCGAGACCTGGTAGGCCCGTATGTTTCGTCTT

a F S H L S S S L Q G L W T I R A Y K A E -

GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTGAGGCTTGGTTCTTG
2761 -----+-----+-----+-----+-----+-----+ 2820
CTCTCCACAGTCCTTGACAACTACGTGTGGTCTAAATGTAAGTCTCCGAACCAAGAAC

a E R C Q E L F D A H Q D L H S E A W F L -

TTTTGACAACGTCCCGCTGGTTGCGCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC
2821 -----+-----+-----+-----+-----+-----+ 2880
AAAAACTGTTGCAGGGCGACCAAGCGGCAGGCAGACCTACGGTAGACACGGTACAAACAG

a F L T T S R W F A V R L D A I C A M F V -

ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACCTCTGGATGCCGGGCAGGTTGGT
2881 -----+-----+-----+-----+-----+-----+ 2940
TAGTAGCAACGGAAACCCAGGGACTAAGACCGTTTTTGAGACCTACGGCCCGTCCAACCA

a I I V A F G S L I L A K T L D A G Q V G -

TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTTCGACAAAGT

Figure 12G

SUBSTITUTE SHEET (RULE 26)

21/56

2941 -----+-----+-----+-----+-----+-----+ 3000
AACCGTGACAGGATACGGGAGTGCGAGTACCCCTACAAAGTCACCACACAAGCTGTTTCA

a L A L S Y A L T L M G M F Q W C V R Q S .

GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA
3001 -----+-----+-----+-----+-----+-----+ 3060
CGACTTCAACTCTTATACTACTAGAGTCATCTTTCCCAGTAACTTATGTGTCTGGAACCT

a A E V E N M M I S V E R V I E Y T D L E .

AAAGAAGCACCTTGGGAATATCAGAAACGCCACCACCAGCCTGGCCCCATGAAGGAGTG
3061 -----+-----+-----+-----+-----+-----+ 3120
TTTCTTCGTGGAACCCTTATAGTCTTTGCGGGTGGTGGTCCGACCGGGGTACTTCCTCAC

a K E A P W E Y Q K R P P P A W P H E G V .

ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT
3121 -----+-----+-----+-----+-----+-----+ 3180
TATTAGAACTGTTACACTTGAAGTACATGTCAGGTCCACCCGGAGACCATGACTTCGTA

a I I F D N V N F M Y S P G G P L V L K H .

CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA
3181 -----+-----+-----+-----+-----+-----+ 3240
GACTGTCGTGAGTAATTTAGTGTTCTTTTCCAACCGTAACACCCTTCTTGGCCTCGACCT

a L T A L I K S Q E K V G I V G R T G A G .

AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT
3241 -----+-----+-----+-----+-----+-----+ 3300
TTTTCAAGGGAGTAGAGTCGGGAAAAATCTAACAGTCTTGGGCTTCCATTTTAAACCTAA

a K S S L I S A L F R L S E P E G K I W I .

GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA
3301 -----+-----+-----+-----+-----+-----+ 3360
CTATTCTAGAACTGTTGACTTTAACCTGAAGTGCTAAATTCCTTCTTTTACAGTTAGTAT

a D K I L T T E I G L H D L R K K M S I I .

CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG
3361 -----+-----+-----+-----+-----+-----+ 3420

Figure 12H

WO 99/49735

PCT/US99/06644

22/56

GGAGTCCTTGGACAAAACAAGTGACCTTGTTACTCCTTTTTGGACCTAGGGAAATTCCTC

a P Q E P V L F T G T M R K N L D P F K E -

CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACCTTAAAGAAACCATTGAA

3421 ----- + ----- + ----- + ----- + ----- + ----- + 3480

GTGTGCCTACTCCTTGACACCTTACGGAATGTTCTCCATGTTGAATTTCTTTGGTAACTT

a H T D E E L W N A L Q E V O L K E T I E -

GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA

3481 ----- + ----- + ----- + ----- + ----- + ----- + 3540

CTAGAAGGACCATTTTACCTATGACTTAATCGTCTTAGTCCTAGGTTAAAATCACAACCT

a D L P G K M D T E L A E S G S N F S V G -

CAAAGACAACCTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT

3541 ----- + ----- + ----- + ----- + ----- + ----- + 3600

GTTTCTGTTGACCACACGGAACGGTCCCGTTAAGAGTCCTTTTTAGTCTATAACTAATAA

a Q R Q L V C L A R A I L R K N Q I L I I -

GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAAATCCGG

3601 ----- + ----- + ----- + ----- + ----- + ----- + 3660

CTACTTCGCTGCCGTTTACACCTAGGTTCTTGACTACTCAATTATGTTTTTTTTTAGGCC

a D E A T A N V D P R T D E L I Q K I R -

GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC

3661 ----- + ----- + ----- + ----- + ----- + ----- + 3720

CTCTTTAAACGGGTGACGTGGCAGGATTGGTAACGTGTGTCTAACTTGTGGTAATAACTG

a E K F A H C T V L T I A H R L N T I I D -

AGCGACAAGATAATGGTTTTAGATTCAAGGAACTGAAAGAATATGATGAGCCGTATGTT

3721 ----- + ----- + ----- + ----- + ----- + ----- + 3780

TCGCTGTTCTATTACAAAATCTAAGTCCTTCTGACTTTCTTATACTACTCGGCATACAA

a S D K I M V L D S G R L K E Y D E P Y V -

TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACCTGGGCAAGGCAGAA

3781 ----- + ----- + ----- + ----- + ----- + ----- + 3840

AACGACGTTTTATTTCTCTCGGATAAAATGTTCTACCACGTTGTTGACCCGTTCCGTCTT

Figure 12I

SUBSTITUTE SHEET (RULE 26)

23/56

a L L Q N K E S L F Y K M V Q Q L G K A E .

GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT
3841 -----+-----+-----+-----+-----+-----+ 3900
CGGCGACGGGAGTGACTTTGTCGTTTTGTCCATATGAAGTTTTCTTTAATAGGTGTATAA

a A A A L T E T A K Q V Y F K R N Y P H I .

GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT
3901 -----+-----+-----+-----+-----+-----+ 3960
CCAGTGTGACTGGTGTACCAATGTTTGTGAAGGTTACCTGTCGGGAGCTGGAATTGATAA

a G H T D H M V T N T S N G Q P S T L T I .

TTCGAGACAGCACTG
3961 -----+----- 3975
AAGCTCTGTCGTGAC

a F E T A L .

Figure 12J

24/56

MOAT C cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

ATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTG
1 -----+-----+-----+-----+-----+-----+ 60
TACTTCCTATAGCTGTATCCTTTTCTCATATAGTAGGGGTCAGGACCCATATCTTCACAC
a M K D I D I G K E Y I I P S P G Y R S V .

AGGGAGAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGA
61 -----+-----+-----+-----+-----+-----+ 120
TCCCTCTCTTGGTCGTGAAGACCCTGCGTGTCTCTGGCACTTCTAAGGTTCAAGTCCTCT
a R E R T S T S G T H R D R E D S K F R R .

ACTCGACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCT
121 -----+-----+-----+-----+-----+-----+ 180
TGAGCTGGCAACCTTACGGTTCTACGGAACCTTTGTCGTCGGGCTCGGCTCCCGGAGAGA
a T R P L E C Q D A L E T A A R A E G L S .

CTTGATGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAAG
181 -----+-----+-----+-----+-----+-----+ 240
GAACTACGGAGGTACGTAAGAGTCGAGTCTTAGGACCTACTCCTCGTAGGGTTCCCTTTC
a L D A S M H S Q L R I L D E E H P K G K .

TACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTCCAAACACCAGCACCCA
241 -----+-----+-----+-----+-----+-----+ 300
ATGGTAGTACCGAACTCACGAGACTTCGGGTAGGCCTGATGAAGGTTTGTGGTCGTGGGT
a Y H H G L S A L K P I R T T S K H Q H P .

GTGGACAATGCTGGGCTTTTTCTGTATGACTTTTTCTGGGCTTTCTTCTCTGGCCCGT
301 -----+-----+-----+-----+-----+-----+ 360
CACCTGTTACGACCCGAAAAAAGGACATACTGAAAAAGCACCGAAAGAAGAGACCGGGCA
a V D N A G L F S C M T F S W L S S L A R .

GTGGCCCAACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAG

Figure 13A

WO 99/49735

PCT/US99/06644

25/56

361 -----+-----+-----+-----+-----+ 420
CACCGGGTGTCTTCCCCCTCGAGAGTTACCTTCTGCACACCAGAGACAGGTTCTGTGCTC

a V A H K K G E L S M E D V W S L S K H E .

TCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTT

421 -----+-----+-----+-----+-----+ 480
AGAAGACTGCACTTGACGTCTTCTGATCTCTCTGACACCGTTCTTCTCGACTTACTTCAA

a S S D V N C R R L E R L W Q E E L N E V .

GGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATC

481 -----+-----+-----+-----+-----+ 540
CCCGGTCTGCGACGAAGGGACGCTTCCCAACACACCTAGAAGACGGCGTGGTCCGAGTAG

a G P D A A S L R R V V W I F C R T R L I .

CTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATG

541 -----+-----+-----+-----+-----+ 600
GACAGGTAGCACACGGACTACTAGTGCCTGACCGACCGAAGTCACCTGGTCGGAAGTAC

a L S I V C L M I T Q L A G F S G P A F M .

GTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTG

601 -----+-----+-----+-----+-----+ 660
CACTTTGTGGAGAACCTCATATGGGTCCGTTGTCTCAGATTGGACGTCATGTGGAACAAC

a V K H L L E Y T Q A T E S N L Q Y S L L .

TTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCAGTCTTGGTCGCTTGCACTGACTTGG

661 -----+-----+-----+-----+-----+ 720
AATCAGACCCGGAGGAGGACTGCCTTTAGCACGCCAGAACCAGCGAACGTGACTGAACC

a L V L G L L L T E I V R S W S L A L T W .

GCATTGAATTACCGAACCAGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAG

721 -----+-----+-----+-----+-----+ 780
CGTAACTTAATGGCTTGCCACAGGCGAACGCCCCCGGTAGGATTGGTACCGTAAATTC

a A L N Y R T G V R L R G A I L T M A F K .

AAGATCCTTAAGTTAAAGAACAATTAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGC

781 -----+-----+-----+-----+-----+ 840

Figure 13B

SUBSTITUTE SHEET (RULE 26)

WO 99/49735

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26/56

TTCTAGGAATTCAATTTCTTGTAATTTCTCTTTAGGGACCCACTCGAGTAGTTGTAAACG

a K I L K L K N I K E K S L G E L I N I C -

TCCAACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGA

841 -----+-----+-----+-----+-----+-----+ 900

AGGTTGCTACCCGCTCTTACAAACTCCGTCGTCGGCAACCGTCGGACGACCGACCTCCT

a S N D G Q R M F E A A A V G S L L A G G -

CCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTC

901 -----+-----+-----+-----+-----+-----+ 960

GGGCAACAACGGTAGAATCCGTACTAAATATTACATTAATAAGACCCTGGTTGTCCGAAG

a P V V A I L G M I Y N V I I L G P T G F -

CTGGGATCAGCTGTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACA

961 -----+-----+-----+-----+-----+-----+ 1020

GACCCTAGTCGACAAAAATAGGAGAAAATGGGTCGTTACTACAAACGTAGTGCCGAGTGT

a L G S A V F I L F Y P A M M F A S R L T -

GCATATTTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAA

1021 -----+-----+-----+-----+-----+-----+ 1080

CGTATAAAGTCCTCTTTTACGCACCGGCGGTGCCTACTTGACAGGTCTTCTACTTACTT

a A Y F R R K C V A A T D E R V Q K M N E -

GTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGT

1081 -----+-----+-----+-----+-----+-----+ 1140

CAAGAATGAATGTAATTTAAATAGTTTTACATACGGACCCAGTTTCGTAAAAGAGTCTCA

a V L T Y I K F I K M Y A W V K A F S Q S -

GTTCAGAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGGGT

1141 -----+-----+-----+-----+-----+-----+ 1200

CAAGTCTTTTAGGCGCTCCTCCTCGCAGCCTATAACCTTTTTTCGGCCCATGAAGGTCCCA

a V Q K I R E E E R R I L E K A G Y F Q G -

ATCACTGTGGGTGTGGCTCCCATTTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTT

1201 -----+-----+-----+-----+-----+-----+ 1260

TAGTGACACCCACACCGAGGGTAACACCACCACTAACGGTCGCACCACTGGAAGAGACAA

Figure 13C

SUBSTITUTE SHEET (RULE 26)

27/56

a I T V G V A P I V V V I A S V V T F S V .
CATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTTCACAGTGGTGACAGTCTTC
1261 -----+-----+-----+-----+-----+ 1320
GTATACTGGGACCCGAAGCTAGACTGTCGTCGTGCCGAAAGTGTCACCACTGTCAGAAG

a H M T L G F D L T A A Q A F T V V T V F .
AATCCATGACTTTTGCTTGAAAGTAACACCGTTTTTCAGTAAAGTCCCTCTCAGAAGCC
1321 -----+-----+-----+-----+-----+ 1380
TTAAGGTACTGAAAACGAACTTTCATTGTGGCAAAAGTCATTTTCAGGGAGAGTCTTCGG

a N S M T F A L K V T P F S V K S L S E A .
TCAGTGGCTGTTGACAGATTTAAGAGTTTGTCTTAATGGAAGAGGTTACATGATAAAG
1381 -----+-----+-----+-----+-----+ 1440
AGTCACCGACAACGTCTAAATTCTCAAACAAAGATTACCTTCTCCAAGTGACTATTTTC

a S V A V D R F K S L F L M E E V H M I K .
AACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGAC
1441 -----+-----+-----+-----+-----+ 1500
TTGTTTGGTCGGTCAGGAGTGAGTTCTATCTCTACTTTTTACGGTGGAACCGTACCCTG

a N K P A S P H I K I E M K N A T L A W D .
TCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAG
1501 -----+-----+-----+-----+-----+ 1560
AGGAGGGTGAGGTCATAGGTCTTGAGCGGGTTCGACTGGGGGTTTTACTTTTTTCTGTTC

a S S H S S I O N S P K L T P K M K K D K .
AGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCG
1561 -----+-----+-----+-----+-----+ 1620
TCCCGAAGGTCCCCGTTCTTTCTCTTCCACTCCGTCGACGTCGCGTGA CTAGTCCGC

a R A S R G K K E K V R Q L Q R T E H Q A .
GTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCAGTCCCGAA
1621 -----+-----+-----+-----+-----+ 1680
CACGACCGTCTCGTCTTTCCGGTGGAGGAGGACCTGTCAGTCTCGCCGGGTCAGGGCTT

Figure 13D

28/56

a V L A E O K G H L L L D S D E R P S P E -
GAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGC
1681 -----+-----+-----+-----+-----+-----+ 1740
CTCCTTCTCCGTTTCGTGTAGGTGGACCCGGTGGACGCGAATGTCTCCTGTGACGTGTCTG

a E E E G K H I H L G H L R L O R T L H S -
ATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGA
1741 -----+-----+-----+-----+-----+-----+ 1800
TAGCTAGACCTCTAGGTTCTCCCATTTGACCAACCTTAGACGCCGTCACACCCTTCACCT

a I D L E I Q E G K L V G I C G S V G S G -
AAAACCTCTCTCATTTAGCCATTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCA
1801 -----+-----+-----+-----+-----+-----+ 1860
TTTTGGAGAGAGTAAAGTCGGTAAAATCCGGTCTACTGCGAAGATCTCCCGTCGTAACGT

a K T S L I S A I L G Q M T L L E G S I A -
ATCAGTGGAACCTTCGCTTATGTGGCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGA
1861 -----+-----+-----+-----+-----+-----+ 1920
TAGTCACCTTGAAGCGAATACACCGGGTCGTCCGGACCTAGGAGTTACGATGAGACTCT

a I S G T F A Y V A Q Q A W I L N A T L R -
GACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACTCTGTGCTGAACAGC
1921 -----+-----+-----+-----+-----+-----+ 1980
CTGTTGTAGGACAAACCCTTCCTTATACTACTTCTTTCTATGTTGAGACACGACTTGTCTG

a D N I L F G K E Y D E E R Y N S V L N S -
TGCTGCCTGAGGCCTGACCTGGCCATTCTTCCAGCAGCGACCTGACGGAGATTGGAGAG
1981 -----+-----+-----+-----+-----+-----+ 2040
ACGACGGACTCCGGACTGGACCGTAAGAAGGGTCGTGCTGGACTGCCTCTAACCTCTC

a C C L R P D L A I L P S S D L T E I G E -
CGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGAT
2041 -----+-----+-----+-----+-----+-----+ 2100
GCTCCTCGGTTGGACTCGCCACCGTCGCGGTCTCCTAGTCGGAACGGGCCCCGGAACATA

a R G A N L S G G O R O R I S L A R A L Y -

Figure 13E

29/56

AGTGACAGGAGCATCTACATCCTGGACGACCCCTCAGTGCCTTAGATGCCCATGTGGGC
2101 -----+-----+-----+-----+-----+-----+ 2160
TCACTGTCCTCGTAGATGTAGGACCTGCTGGGGGAGTCACGGAATCTACGGGTACACCCG

a S D R S I Y I L D D P L S A L D A H V G -

AACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGT
2161 -----+-----+-----+-----+-----+-----+ 2220
TTGGTGTAGAAGTTATCACGATAGGCCTTTGTAGAGTTCAGGTTCTGTCAAGACAAACAA

a N H I F N S A I R K H L K S K T V L F V -

ACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGT
2221 -----+-----+-----+-----+-----+-----+ 2280
TGGGTGGTCAATGTCATGGACCAACTGACACTACTTCACTAGAAGTACTTTCTCCCGACA

a T H Q L Q Y L V D C D E V I F M K E G C -

ATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATT
2281 -----+-----+-----+-----+-----+-----+ 2340
TAATGCCTTTCTCCGTGGGTACTCCTTGACTACTTAAATTTACCACTGATACGATGGTAA

a I T E R G T H E E L M N L N G D Y A T I -

TTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACC
2341 -----+-----+-----+-----+-----+-----+ 2400
AAATTATTGGACAACGACCCTCTCTGTGGCGGTCAACTCTAGTTAAGTTTTTCTTTGG

a F N N L L L G E T P P V E I N S K K E T -

AGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCTTAAACAGGATCAGTAAAGAAGGAA
2401 -----+-----+-----+-----+-----+-----+ 2460
TCACCAAGTGTCTTCTTCAGTGTTCTGTTCCAGGATTTTGTCTAGTCATTTCTTCCTT

a S G S Q K K S Q D K G P K T G S V K K E -

AAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCA
2461 -----+-----+-----+-----+-----+-----+ 2520
TTTCGTCATTTCCGGTCTCCTTCCCGTCGAACACGTCGACCTTCTCTTTCCCGTCCCAAGT

a K A V K P E E G Q L V Q L E E K G Q G S -

Figure 13F

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GTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCTTGGCATTCTG
 2521 -----+-----+-----+-----+-----+-----+ 2580
 CACGGGACCAGTCATATACCACAGATGTAGGTCCGACGACCCCCGGGAACCGTAAGGAC

a V P W S V Y G V Y I Q A A G G P L A F L .

GTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTG
 2581 -----+-----+-----+-----+-----+-----+ 2640
 CAATAATACCGGGAAGTACGACTTACATCCGTCGTGGCGGAAGTCGTGGACCACCAAC

a V I M A L F M L N V G S T A F S T W W L .

AGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCG
 2641 -----+-----+-----+-----+-----+-----+ 2700
 TCAATGACCTAGTTCGTTCTTCGCCCTTGTGGTGACACTGAGCTCCCTTGCTCTGGAGC

a S Y W I K Q G S G N T T V T R G N E T S .

GTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTC
 2701 -----+-----+-----+-----+-----+-----+ 2760
 CACTCACTGTCGTA CTCTCTGTTAGGAGTATACGTCATGATACGGTCGTAGATGCGGGAG

a V S D S M K D N P H M Q Y Y A S I Y A L .

TCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACG
 2761 -----+-----+-----+-----+-----+-----+ 2820
 AGGTACCGTCAGTACGACTAGGACTTTGCGTAAGCTCCTCAACAGAAACAGTTCCCGTGC

a S M A V M L I L K A I R G V V F V K G T .

CTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATG
 2821 -----+-----+-----+-----+-----+-----+ 2880
 GACGCTCGAAGGAGGGCCGACGTA CTGCTCGAAAAGGCTTCCTAGGAAGCTTCGGGATAC

a L R A S S R L H D E L F R R I L R S P M .

AAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGAT
 2881 -----+-----+-----+-----+-----+-----+ 2940
 TTCAAAAAACTGTGCTGGGGGTGTCCCTCCTAAGAGTTGTCCAAAAGGTTTCTGTACCTA

a K F F D T T P T G R I L N R F S K D M D .

GAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTTCATCCAGAACGTTATCCTGGTG

Figure 13G

SUBSTITUTE SHEET (RULE 26)

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2941 -----+-----+-----+-----+-----+-----+ 3000
 CTTCAACTGCACGCCGACGGCAAGGTCCGGCTCTACAAGTAGGTCTTGCAATAGGACCAC

a E V D V R L P F Q A E M F I Q N V I L V -

TTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCC
 3001 -----+-----+-----+-----+-----+ 3060
 AAGAAGACACACCCTTACTAGCGTCCTCAGAAGGGCACCAAGGAACACCGTCACCCCGGG

a F F C V G M I A G V F P W F L V A V G P -

CTTGTCACTCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCTGATTCGGGAGCTGAAG
 3061 -----+-----+-----+-----+-----+ 3120
 GAACAGTAGGAGAAAAGTCAGGACGTGTAACAGAGGTCCCAGGACTAAGCCCTCGACTTC

a L V I L F S V L H I V S R V L I R E L K -

CGTCTGGACAATATCACGCAGTCACCTTCTCTCCACATCACGTCCAGCATAACAGGGC
 3121 -----+-----+-----+-----+-----+ 3180
 GCAGACCTGTTATAGTGCGTCAGTGGAAAGGAGAGGGTGTAGTGCAGGTCGTATGTCCCG

a R L D N I T Q S P F L S H I T S S I Q G -

CTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTG
 3181 -----+-----+-----+-----+-----+ 3240
 GAACGGTGGTAGGTGCGGATGTTATTTCCCGTCCTCAAAGACGTGTCTATGGTCCTCGAC

a L A T I H A Y N K G Q E F L H R Y Q E L -

CTGGATGACAACCAAGCTCCTTTTTTTTTTGTTCACGTGTGCGATGCGGTGGCTGGCTGTG
 3241 -----+-----+-----+-----+-----+ 3300
 GACCTACTGTTGGTTCGAGGAAAAAAAAACAAATGCACACGCTACGCCACCGACCGACAC

a L D D N Q A P F F L F T C A M R W L A V -

CGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATG
 3301 -----+-----+-----+-----+-----+ 3360
 GCCGACCTGGAGTAGTCGTAGCGGGAGTAGTGGTGGTGCCCCGACTACTAGCAAGAATAC

a R L D L I S I A L I T T T G L M I V L M -

CACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACG
 3361 -----+-----+-----+-----+-----+ 3420

Figure 13H

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GTGCCCCGTCTAAGGGGGTCGGATACGCCCAGAGCGGTAGAGAATACGACAGGTCAATTGC

a H G O I P P A Y A G L A I S Y A V O L T .

GGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTACCTCGGTG
 3421 ----- + ----- + ----- + ----- + ----- + ----- + 3480
 CCCGACAAGGTCAAATGCCAGTCTGACCGTAGACTCTGTCTTCGAGCTAAGTGGAGCCAC

a G L F O F T V R L A S E T E A R F T S V .

GAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAAC
 3481 ----- + ----- + ----- + ----- + ----- + ----- + 3540
 CTCTCCTAGTTAGTGATGTAATTCTGAGACAGGAACCTTCGTGGACGGTCTTAATTCTTG

a E R I N H Y I K T L S L E A P A R I K N .

AAGGCTCCCTCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATG
 3541 ----- + ----- + ----- + ----- + ----- + ----- + 3600
 TTCCGAGGGAGGGGACTGACCGGGGTCTCCCTCTCCACTGGAACTCTTGCGTCTCTAC

a K A P S P D W P Q E G E V T F E N A E M .

AGGTACCGAGAAAACCTCCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAA
 3601 ----- + ----- + ----- + ----- + ----- + ----- + 3660
 TCCATGGCTCTTTTGGAGGGAGAACAGGATTTCTTTCATAGGAAGTGCTAGTTTGGATT

a R Y R E N L P L V L K K V S F T I K P K .

GAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTC
 3661 ----- + ----- + ----- + ----- + ----- + ----- + 3720
 CTCTTCTAACCGTAACACCCCGCCTGTCTAGTCCCTTCAGGAGCGACCCCTACCGGGAG

a E K I G I V G R T G S G K S S L G M A L .

TTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGAT
 3721 ----- + ----- + ----- + ----- + ----- + ----- + 3780
 AAGGCAGACCACCTCAATAGACCTCCGACGTAGTTCTAACTACCTCACTCTTAGTCACTA

a F R L V E L S G G C I K I D G V R I S D .

ATTGGCCTTGCCGACCTCCGAAGCAAACCTCTCTATCATTCCTCAAGAGCCGGTGCTGTTT
 3781 ----- + ----- + ----- + ----- + ----- + ----- + 3840
 TAACCGGAACGGCTGGAGGCTTCGTTTGAGAGATAGTAAGGAGTTCTCGGCCACGACAAG

Figure 131

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a I G L A D L R S K L S I I P Q E P V L F -
 AGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGG
 3841 -----+-----+-----+-----+-----+ 3900
 TCACCGTGACAGTCTAGTTTAAACCTGGGGAAGTTGGTCATGTGACTTCTGGTCTAAACC

a S G T V R S N L D P F N O Y T E D Q I W -
 GATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAA
 3901 -----+-----+-----+-----+-----+ 3960
 CTACGGGACCTCTCCTGTGTGTACTTTCTTACATAACGAGTCGATGGAGACTTTGAACTT

a D A L E R T H M K E C I A Q L P L K L E -
 TCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATA
 3961 -----+-----+-----+-----+-----+ 4020
 AGACTTCACTACCTCTTACCCCTATTGAAGAGTCACCCCTTGCCGTCGAGAACACGTAT

a S E V M E N G D N F S V G E R Q L L C I -
 GCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATG
 4021 -----+-----+-----+-----+-----+ 4080
 CGATCTCGGGACGAGGCGGTGACATTCTAAGACTAAATCTACTTCGGTGTGACGGTAC

a A R A L L R H C K I L I L D E A T A A M -
 GACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTCAGACTGTACC
 4081 -----+-----+-----+-----+-----+ 4140
 CTGTGTCTCTGTCTGAATAACTAAGTTCTCTGGTAGGCTCTTCGTAAACGTCTGACATGG

a D T E T D L L I Q E T I R E A F A D C T -
 ATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTG
 4141 -----+-----+-----+-----+-----+ 4200
 TACGACTGGTAACGGGTAGCGGACGTGTGCCAAGATCCGAGGCTATCCTAATACCACGAC

a M L T I A H R L H T V L G S D R I M V L -
 GCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCC
 4201 -----+-----+-----+-----+-----+ 4260
 CGGGTCCCTGTCCACCACCTCAAACGTGTGGGGTAGCCAGGAAGACAGGTTGCTGTCAAGG

Figure 13J

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a A Q G Q V V E F D T P S V L L S N D S S .

CGATTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGA
4261 -----+-----+-----+-----+-----+---- 4314
GCTAAGATACGGTACAAACGACGACGTCTCTTGTTCAGCGACAGTTCCCGACT

a R F Y A M F A A A E N K V A V K G .

Figure 13K

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MOAT D cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

ATGGACGCCCTGTGCGGTTCCGGGGAGCTCGGCTCCAAGTTCTGGGACTCCAACCTGTCT
1 -----+-----+-----+-----+-----+-----+ 60
TACCTGCGGGACACGCCAAGGCCCTCGAGCCGAGGTTCAAGACCCTGAGGTTGGACAGA

a M D A L C G S G E L G S K F W D S N L S .

GTGCACACAGAAAACCCGGACCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCCTGGGTG
61 -----+-----+-----+-----+-----+-----+ 120
CACGTGTGTCTTTTGGGCTGGAGTGAGGGACGAAGGTCTTGAGGGACGACCGGACCCAC

a V H T E N P D L T P C F Q N S L L A W V .

CCCTGCATCTACCTGTGGGTCGCCCTGCCCTGCTACTTGCTCTACCTGCGGCACCATTTGT
121 -----+-----+-----+-----+-----+-----+ 180
GGGACGTAGATGGACACCCAGCGGGACGGGACGATGAACGAGATGGACGCCGTGGTAACA

a P C I Y L W V A L P C Y L L Y L R H H C .

CGTGGCTACATCATCCTCTCCCACCTGTCCAAGCTCAAGATGGTCCTGGGTGTCCTGCTG
181 -----+-----+-----+-----+-----+-----+ 240
GCACCGATGTAGTAGGAGAGGGTGGACAGGTTCTGAGTTCTACCAGGACCCACAGGACGAC

a R G Y I I L S H L S K L K M V L G V L L .

TGGTGCGTCTCCTGGGCGGACCTTTTTTACTCCTTCCATGGCCTGGTCCATGGCCGGGCC
241 -----+-----+-----+-----+-----+-----+ 300
ACCACGCAGAGGACCCGCCTGGAAAAAATGAGGAAGGTACCGGACCAGGTACCGGCCCGG

a W C V S W A D L F Y S F H G L V H G R A .

CCTGCCCTGTTTTCTTTGTCACCCCTTGGTGGTGGGGGTCACCATGCTGCTGGCCACC
301 -----+-----+-----+-----+-----+-----+ 360
GGACGGGGACAAAAGAAACAGTGGGGGAACCACCACCCCAAGTGGTACGACGACCGGTGG

a P A P V F F V T P L V V G V T M L L A T .

CTGCTGATACAGTATGAGCGGCTGCAGGGCGTACAGTCTTCGGGGGTCCTCATTATCTTC

Figure 14A

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361 -----+-----+-----+-----+-----+-----+ 420
 GACGACTATGTCATACTCGCCGACGTCCCGCATGTCAGAAGCCCCCAGGAGTAATAGAAG

a L L I Q Y E R L Q G V Q S S G V L I I F -

TGGTTCCTGTGTGTGGTCTGCGCCATCGTCCCATTCGCTCCAAGATCCTTTAGCCAAG

421 -----+-----+-----+-----+-----+-----+ 480
 ACCAAGGACACACACCAGACGCGGTAGCAGGGTAAGGCGAGGTTCTAGGAAAATCGGTTTC

a W F L C V V C A I V P F R S K I L L A K -

GCAGAGGGTGAGATCTCAGACCCCTTCCGCTTCACCACCTTCTACATCCACTTTGCCCTG

481 -----+-----+-----+-----+-----+-----+ 540
 CGTCTCCCACTCTAGAGTCTGGGGAAGGCGAAGTGGTGGAAGATGTAGGTGAAACGGGAC

a A E G E I S D P F R F T T F Y I H F A L -

GTACTCTCTGCCCTCATCTTGGCCTGCTTCAGGGAGAAACCTCCATTTTCTCCGCAAAG

541 -----+-----+-----+-----+-----+-----+ 600
 CATGAGAGACGGGAGTAGAACC GGACGAAGTCCCTCTTTGGAGGTAAAAAGAGGCGTTTC

a V L S A L I L A C F R E K P P F F S A K -

AATGTCGACCCTAACCCTACCCTGAGACCAGCGCTGGCTTTCTCTCCCGCCTGTTTTTC

601 -----+-----+-----+-----+-----+-----+ 660
 TTACAGCTGGGATTGGGGATGGGACTCTGGTCGCGACCGAAAGAGAGGGCGGACAAAAAG

a N V D P N P Y P E T S A G F L S R L F F -

TGGTGGTTCACAAAGATGGCCATCTATGGCTACCGGCATCCCCTGGAGGAGAAGGACCTC

661 -----+-----+-----+-----+-----+-----+ 720
 ACCACCAAGTGTTCCTACCGGTAGATACCGATGGCCGTAGGGGACCTCCTCTTCCTGGAG

a W W F T K M A I Y G Y R H P L E E K D L -

TGGTCCCTAAAGGAAGAGGACAGATCCCAGATGGTGGTGCAGCAGCTGCTGGAGGCATGG

721 -----+-----+-----+-----+-----+-----+ 780
 ACCAGGGATTTCCTTCTCCTGTCTAGGGTCTACCACCACGTCGTCGACGACCTCCGTACC

a W S L K E E D R S Q M V V Q Q L L E A W -

AGGAAGCAGGAAAAGCAGACGGCACGACACAAGGCTTCAGCAGCACCTGGGAAAAATGCC

781 -----+-----+-----+-----+-----+-----+ 840

Figure 14B

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TCCTTCGTCCTTTTCGTCTGCCGTGCTGTGTTCCGAAGTCGTCTGGACCCTTTTACGG

a R K Q E K Q T A R H K A S A A P G K N A -

TCCGGCGAGGACGAGGTGCTGCTGGGTGCCCGGCCAGGCCCGGAAGCCCTCCTTCCTG

841 -----+-----+-----+-----+-----+-----+ 900

AGGCCGCTCCTGCTCCACGACGACCCACGGGCCGGTCCGGGGCCTTCGGGAGGAAGGAC

a S G E D E V L L G A R P R P R K P S F L -

AAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCATCAGTGCCTGCTTCAAGCTTATC

901 -----+-----+-----+-----+-----+-----+ 960

TTCCGGGACGACCGGTGGAAGCCGAGGTGGAAGGAGTAGTCACGGACGAAGTTCGAATAG

a K A L L A T F G S S F L I S A C F K L I -

CAGGACCTGCTCTCCTTCATCAATCCACAGCTGCTCAGCATCCTGATCAGGTTTATCTCC

961 -----+-----+-----+-----+-----+-----+ 1020

GTCCTGGACGAGAGGAAGTAGTTAGGTGTGACGAGTCGTAGGACTAGTCCAAATAGAGG

a Q D L L S F I N P Q L L S I L I R F I S -

AACCCCATGGCCCCCTCCTGGTGGGGCTTCCTGGTGGCTGGGGCTGATGTTCTGTGCTCC

1021 -----+-----+-----+-----+-----+-----+ 1080

TTGGGGTACCGGGGGAGGACCACCCGAAGGACCACCGACCCGACTACAAGGACACGAGG

a N P M A P S W W G F L V A G L M F L C S -

ATGATGCAGTCGCTGATCTTACAACACTATTACCACTACATCTTTGTGACTGGGGTGAAG

1081 -----+-----+-----+-----+-----+-----+ 1140

TACTACGTCAGCGACTAGAATGTTGTGATAATGGTGTATGTAGAAACACTGACCCCACTTC

a M M Q S L I L Q H Y Y H Y I F V T G V K -

TTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCTGGTTATCACCAACTCAGTC

1141 -----+-----+-----+-----+-----+-----+ 1200

AAAGCATGACCCTAGTACCCACAGTAGATGTCCTTCCGAGACCAATAGTGGTTGAGTCAG

a F R T G I M G V I Y R K A L V I T N S V -

AAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTCAGTGGATGCCAGCGCTTC

1201 -----+-----+-----+-----+-----+-----+ 1260

TTTGACGCGAGGTGACACCCCTTTAACAGTTGGAGTACAGTCACCTACGGGTCGCGAAG

Figure 14C

- a K R A S T V G E I V N L M S V D A Q R F .
ATGGACCTTGCCCCCTTCCTCAATCTGCTGTGGTCAGCACCCCTGCAGATCATCCTGGCG
1261 -----+-----+-----+-----+-----+-----+ 1320
TACCTGGAACGGGGAAGGAGTTAGACGACACCAGTCGTGGGGACGTCTAGTAGGACCGC
- a M D L A P F L N L L W S A P L Q I I L A .
ATCTACTTCCTCTGGCAGAACCTAGGTCCCTCTGTCCTGGCTGGAGTCGCTTTCATGGTC
1321 -----+-----+-----+-----+-----+-----+ 1380
TAGATGAAGGAGACCGTCTTGGATCCAGGGAGACAGGACCGACCTCAGCGAAAGTACCAG
- a I Y F L W Q N L G P S V L A G V A F M V .
TTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCGCGCCTTCCAGGTAAAGCAA
1381 -----+-----+-----+-----+-----+-----+ 1440
AACGACTAAGGTGAGTTGCCTCGACACCGGCACTTCTACGCGCGGAAGGTCCATTTTCGTT
- a L L I P L N G A V A V K M R A F Q V K Q .
ATGAAATTGAAGGACTCGCGCATCAAGCTGATGAGTGAGATCCTGAACGGCATCAAGGTG
1441 -----+-----+-----+-----+-----+-----+ 1500
TACTTTAACTTCCTGAGCGCGTAGTTCGACTACTCACTCTAGGACTTGCCGTAGTTCAC
- a M K L K D S R I K L M S E I L N G I K V .
CTGAAGCTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGTGGAGGGCATCCGGCAGGGT
1501 -----+-----+-----+-----+-----+-----+ 1560
GACTTCGACATGCGGACCCTCGGGTCGAAGGACTTCGTCCACCTCCCGTAGGCCGTCCCA
- a L K L Y A W E P S F L K Q V E G I R Q G .
GAGCTCCAGCTGCTGCGCACGGCGGCCTACCTCCACACCACAACCACCTTCACCTGGATG
1561 -----+-----+-----+-----+-----+-----+ 1620
CTCGAGGTGACGACGCGTGCCGCCGATGGAGGTGTGGTGTTGGTGGAAGTGGACCTAC
- a E L Q L L R T A A Y L H T T T T F T W M .
TGCAGCCCCTTCCTGGTGACCCTGATCACCTCTGGGTGTACGTGTACGTGGACCCAAAC
1621 -----+-----+-----+-----+-----+-----+ 1680
ACGTGCGGGAAGGACCACTGGGACTAGTGGGAGACCCACATGCACATGCACCTGGGTTTG

Figure 14D

a C S P F L V T L I T L W V Y V Y V D P N -
AATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCTTGTTAATATCTTAAGACTT
1681 -----+-----+-----+-----+-----+-----+ 1740
TTACACGACCTGCGGCTCTTCCGGAAACACAGACACAGGAACAAATTATAGAATTCTGAA

a N V L D A E K A F V S V S L F N I L R L -
CCCCCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCAGGCCAGTGTGTCTCTGAAA
1741 -----+-----+-----+-----+-----+-----+ 1800
GGGGAGTTGTACGACGGGGTCAATTAGTCGTTGGACTGAGTCCGGTCACACAGAGACTTT

a P L N M L P Q L I S N L T Q A S V S L K -
CGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCAGAGTGTGGAAAGAAAGACC
1801 -----+-----+-----+-----+-----+-----+ 1860
GCCTAGGTCGTTAAGGACTCGGTTCTCCTTGAAGTGGGGTCTCACACCTTTCTTTCTGG

a R I Q Q F L S Q E E L D P Q S V E R K T -
ATCTCCCCAGGCTATGCCATCACCATACACAGTGGCACCTTCACCTGGGCCCAGGACCTG
1861 -----+-----+-----+-----+-----+-----+ 1920
TAGAGGGGTCCGATACGGTAGTGGTATGTGTACCGTGGAAGTGGACCCGGGTCTGGAC

a I S P G Y A I T I H S G T F T W A Q D L -
CCCCCACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGCACTGGTGGCCGTGGTG
1921 -----+-----+-----+-----+-----+-----+ 1980
GGGGGGTGAGACGTGTGCGATCTGTAGGTCCAGGGCTTTCCCCGTGACCACCGGCACCAC

a P P T L H S L D I Q V P K G A L V A V V -
GGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGTGTCTGCCCTGCTGGGAGAGATGGAGAAG
1981 -----+-----+-----+-----+-----+-----+ 2040
CCCGGACACCCGACACCCTTCAGGAGGGACCACAGACGGGACGACCCTCTCTACCTCTTC

a G P V G C G K S S L V S A L L G E M E K -
CTAGAAGGCCAAAGTGACATGAAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTG
2041 -----+-----+-----+-----+-----+-----+ 2100
GATCTTCCGTTTCACGTGTACTTCCGTACCTAGGTCTTGACGTGAGAAGTCCTTTTGAC

a L E G K V H M K A W I Q N C T L Q E N V -

Figure 14E

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CTTTTCGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTG
2101 -----+-----+-----+-----+-----+-----+ 2160
GAAAAGCCGTTTCGGGACTTGGGGTTCGCGATGGTCGTCTGAGACCTCCGGACACGGAAC

a L F G K A L N P K R Y Q Q T L E A C A L -

CTAGCTGACCTGGAGATGCTGCCTGGTGGGGATCAGACAGAGATTGGAGAGAAGGGCATT
2161 -----+-----+-----+-----+-----+-----+ 2220
GATCGACTGGACCTCTACGACGGACCAACCCCTAGTCTGTCTCTAACCTCTCTCCCGTAA

a L A D L E M L P G G D Q T E I G E K G I -

AACCTGTCTGGGGGCCAGCGGCAGCGGGTCAGTCTGGCTCGAGCTGTTTACAGTGATGCC
2221 -----+-----+-----+-----+-----+-----+ 2280
TTGGACAGACCCCCGGTCGCCGTCGCCAGTCAGACCGAGCTCGACAAATGTCACTACGG

a N L S G G Q R Q R V S L A R A V Y S D A -

GATATTTTCTTGCTGGATGACCCACTGTCCGCGGTGGACTCTCATGTGGCCAAGCACATC
2281 -----+-----+-----+-----+-----+-----+ 2340
CTATAAAAGAACGACCTACTGGGTGACAGGCGCCACCTGAGAGTACACCGGTTTCGTGTAG

a D I F L L D D P L S A V D S H V A K H I -

TTTGACCACGTCATCGGGCCAGAAGGCGTGCTGGCAGGCAAGACGCGAGTGCTGGTGACG
2341 -----+-----+-----+-----+-----+-----+ 2400
AAACTGGTGCAGTAGCCCGGTCTTCCGCACGACCGTCCGTTCTGCGCTCACGACCACTGC

a F D H V I G P E G V L A G K T R V L V T -

CACGGCATTAGCTTCCTGCCCCAGACAGACTTCATCATTGTGCTAGCTGATGGACAGGTG
2401 -----+-----+-----+-----+-----+-----+ 2460
GTGCCGTAATCGAAGGACGGGGTCTGTCTGAAGTAGTAACACGATCGACTACCTGTCCAC

a H G I S F L P Q T D F I I V L A D G Q V -

TCTGAGATGGGCCCCGTACCCAGCCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTC
2461 -----+-----+-----+-----+-----+-----+ 2520
AGACTCTACCCGGGCATGGGTCTGGGACGACGTGCGGTTGCCGAGGAAACGGTTGAAAGAG

a S E M G P Y P A L L Q R N G S F A N F L -

Figure 14F

SUBSTITUTE SHEET (RULE 26)

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TGCAACTATGCCCCGATGAGGACCAAGGGCACCTGGAGGACAGCTGGACCGCGTTGGAA
 2521 ----- + ----- + ----- + ----- + ----- + ----- + 2580
 ACGTTGATACGGGGGCTACTCCTGGTTCCCGTGGACCTCCTGTCGACCTGGCGCAACCTT
 a C N Y A P D E D Q G H L E D S W T A L E .

GGTGCAGAGGATAAGGAGGCACTGCTGATTGAAGACACACTCAGCAACCACACGGATCTG
 2581 ----- + ----- + ----- + ----- + ----- + ----- + 2640
 CCACGTCTCCTATTCTCCTCCGTGACGACTAACTTCTGTGTGAGTCGTTGGTGTGCCTAGAC
 a G A E D K E A L L I E D T L S N H T D L .

ACAGACAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCC
 2641 ----- + ----- + ----- + ----- + ----- + ----- + 2700
 TGTCTGTTACTAGGTCACTGGATACACCAGGTCTTCGTCAAATACTCTGTGCACTCACGG
 a T D N D P V T Y V V Q K Q F M R Q L S A .

CTGTCCTCAGATGGGGAGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCA
 2701 ----- + ----- + ----- + ----- + ----- + ----- + 2760
 GACAGGAGTCTACCCCTCCCTGTCCCAGCCGGACATGGGGCCTCCGTGGACCCAGGTAGT
 a L S S D G E G Q G R P V P R R H L G P S .

GAGAAGGTGCAGGTGACAGAGGCGAAGGCAGATGGGGCACTGACCCAGGAGGAGAAAGCA
 2761 ----- + ----- + ----- + ----- + ----- + ----- + 2820
 CTCTTCACGTCCACTGTCTCCGCTTCCGTCTACCCCGTGACTGGGTCCTCCTCTTTCTGT
 a E K V Q V T E A K A D G A L T Q E E K A .

GCCATTGGCACTGTGGAGCTCAGTGTGTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGT
 2821 ----- + ----- + ----- + ----- + ----- + ----- + 2880
 CGGTAACCGTGACACCTCGAGTCACACAAGACCCTAATACGGTTCGGGCACCCCGAGACA
 a A I G T V E L S V F W D Y A K A V G L C .

ACCACGCTGGCCATCTGTCTCCTGTATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAAT
 2881 ----- + ----- + ----- + ----- + ----- + ----- + 2940
 TGGTGCGACCGGTAGACAGAGGACATACCCAGTTTCACGCCGACGGTAACCTCGGTTA
 a T T L A I C L L Y V G Q S A A A I G A N

GTGTGGCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACAACACTTCC

Figure 14G

2941 -----+-----+-----+-----+-----+-----+ 3000
 CACACCGAGTCACGGACCTGTTTACTACGGTACCGTCTGTCATCTGTCTTGTGTGAAGG
 a V W L S A W T N D A M A D S R O N N T S .
 CTGAGGCTGGGCGTCTATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCA
 3001 -----+-----+-----+-----+-----+-----+ 3060
 GACTCCGACCCGCAGATACGACGAAATCCTTAAGACGTTCCCAAGAACCACTACGACCGT
 a L R L G V Y A A L G I L Q G F L V M L A .
 GCCATGGCCATGGCAGCGGGTGGCATCCAGGCTGCCCCTGTGTTGCACCAGGCACTGCTG
 3061 -----+-----+-----+-----+-----+-----+ 3120
 CGGTACCGGTACCGTCGCCCACCGTAGGTCCGACGGGCACACAACGTGGTCCGTGACGAC
 a A M A M A A G G I O A A R V L H Q A L L -
 CACAACAAGATACGCTCGCCACAGTCCTTCTTTGACACCACACCATCAGGCCGCATCCTG
 3121 -----+-----+-----+-----+-----+-----+ 3180
 GTGTTGTTCTATGCGAGCGGTGTCAGGAAGAACTGTGGTGTGGTAGTCCGGCGTAGGAC
 a H N K I R S P Q S F F D T T P S G R I L -
 AACTGCTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATG
 3181 -----+-----+-----+-----+-----+-----+ 3240
 TTGACGAAGAGGTTCTGTAGATACAGCAACTACTCCAAGACCGGGGACAGTAGGAGTAC
 a N C F S K D I Y V V D E V L A P V I L M -
 CTGCTCAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCG
 3241 -----+-----+-----+-----+-----+-----+ 3300
 GACGAGTTAAGGAAGAAGTTGCGGTAGAGGTGAGAACACCAGTAGTACCGGTCGTGCGGC
 a L L N S F F N A I S T L V V I M A S T P -
 CTCTTCACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTAT
 3301 -----+-----+-----+-----+-----+-----+ 3360
 GAGAAGTGACACCAGTAGGACGGGGACCGACACGAGATGTGGAATCACGTCGCGAAGATA
 a L F T V V I L P L A V L Y T L V Q R F Y -
 GCAGCCACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCC
 3361 -----+-----+-----+-----+-----+-----+ 3420

Figure 14H

CGTCGGTGTAGTGCCGTTGACTTCGCCGACCTTAGTCAGTCGGCGAGTGGATAGATGAGG

a A A T S R O L K R L E S V S R S P I Y S .

CACTTTTCGGAGACAGTGACTGGTGCCAGTGTTCATCCGGGCCTACAACCGCAGCCGGGAT
3421 -----+-----+-----+-----+-----+-----+ 3480
GTGAAAAGCCTCTGTCACTGACCACGGTCACAGTAGGCCCGGATGTTGGCGTCGGCCCTA

a H F S E T V T G A S V I R A Y N R S R D .

TTTGAGATCATCAGTGATACTAAGGTGGATGCCAACCAGAGAAGCTGCTACCCCTACATC
3481 -----+-----+-----+-----+-----+-----+ 3540
AAACTCTAGTAGTCACTATGATTCCACCTACGGTTGGTCTCTTCGACGATGGGGATGTAG

a F E I I S D T K V D A N Q R S C Y P Y I .

ATCTCCAACCGGTGGCTGAGCATCGGAGTGGAGTTTCGTGGGGAACTGCGTGGTGCTCTTT
3541 -----+-----+-----+-----+-----+-----+ 3600
TAGAGGTTGGCCACCGACTCGTAGCCTCACCTCAAGCACCCCTTGACGCACCACGAGAAA

a I S N R W L S I G V E F V G N C V V L F .

GCTGCACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCT
3601 -----+-----+-----+-----+-----+-----+ 3660
CGACGTGATAAACGGCAGTAGCCCTCCTCGTCGGACTTGGGCCCCGACCACCCGGAAAGA

a A A L F A V I G R S S L N P G L V G L S .

GTGTCCTACTCCTTGACAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGAT
3661 -----+-----+-----+-----+-----+-----+ 3720
CACAGGATGAGGAACGTCCACTGTAAACGAGACTTGACCTACTATGCTTACTACAGTCTA

a V S Y S L Q V T F A L N W M I R M M S D .

TTGGAATCTAACATCGTGGCTGTGGAGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAG
3721 -----+-----+-----+-----+-----+-----+ 3780
AACCTTAGATTGTAGCACCGACACCTCTCCAGTTCTCATGAGGTTCTGTCTCTGTCTC

a L E S N I V A V E R V K E Y S K T E T E .

CGGCCCTGGGTGGTGGAAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCACGTGGGGAGGTG
3781 -----+-----+-----+-----+-----+-----+ 3840
CGCGGGACCCACCACCTCCGTCGGCGGGAGGGCTTCCAACCGGGGGTGCACCCCTCCAC

Figure 14I

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a A P W V V E G S R P P E G W P P R G E V .

GAGTTCCGGAATTATTCTGTGCGCTACCGGCCGGCCTAGACCTGGTGCTGAGAGACCTG
3841 -----+-----+-----+-----+-----+-----+ 3900
CTCAAGGCCTTAATAAGACACGCGATGGCCGGCCGGATCTGGACCACGACTCTCTGGAC

a E F R N Y S V R Y R P G L D L V L R D L .

AGTCTGCATGTGCACGGTGGCGAGAAGGTGGGGATCGTGGGCCGCACTGGGGCTGGCAAG
3901 -----+-----+-----+-----+-----+-----+ 3960
TCAGACGTACACGTGCCACCGCTCTTCCACCCCTAGCACCCGGCGTGACCCCGACCGTTC

a S L H V H G G E K V G I V G R T G A G K .

TCTTCCATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATT
3961 -----+-----+-----+-----+-----+-----+ 4020
AGAAGGTACTGGGAAACGGACAAGGCGTAGGACCTCCGCCGTTTCCCACTTTAGGCGTAA

a S S M T L C L F R I L E A A K G E I R I .

GATGGCCTCAATGTGGCAGACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATC
4021 -----+-----+-----+-----+-----+-----+ 4080
CTACCGGAGTTACACCGTCTGTAGCCGGAGGTACTGGACGCGAGAGTCGACTGGTAGTAG

a D G L N V A D I G L H D L R S Q L T I I .

CCGCAGGACCCCATCCTGTTCTCGGGGACCCTGCGCATGAACCTGGACCCCTTCGGCAGC
4081 -----+-----+-----+-----+-----+-----+ 4140
GGCGTCTTGGGGTAGGACAAGAGCCCCTGGGACGCGTACTTGGACCTGGGGAAGCCGTCG

a P Q D P I L F S G T L R M N L D P F G S .

TACTCAGAGGAGGACATTTGGTGGGCTTTGGAGCTGTCCACCTGCACACGTTTGTGAGC
4141 -----+-----+-----+-----+-----+-----+ 4200
ATGAGTCTCCTCCTGTAAACCAACCGAAACCTCGACAGGGTGGACGTGTGCAAACACTCG

a Y S E E D I W W A L E L S H L H T F V S .

TCCAGCCGGCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGC
4201 -----+-----+-----+-----+-----+-----+ 4260
AGGGTCGGCCGTCCGGACCTGAAGGTCACGAGTCTCCCGCCCCTCTTAGAGTCGCACCCG

Figure 14J

a S Q P A G L D F Q C S E G G E N L S V G -
CAGAGGCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTA
4261 ----- + ----- + ----- + ----- + ----- + ----- + 4320
GTCTCCGTCGAGCACACGGACCGGGCTCGGGACGAGGCGTTCTCGGCGTAGGACCAAAAT

a Q R Q L V C L A R A L L R K S R I L V L -
GACGAGGCCACACCTGCCATCGACCTGGAGACTGACAACCTCATCCAGGCTACCATCCGC
4321 ----- + ----- + ----- + ----- + ----- + ----- + 4380
CTGCTCCGGTGTGACGGTAGCTGGACCTCTGACTGTTGGAGTAGGTCCGATGGTAGGCG

a D E A T A A I D L E T D N L I Q A T I R -
ACCCAGTTTGATACCTGCACTGTCCTGACCATCGCACACCGGCTTAACACTATCATGGAC
4381 ----- + ----- + ----- + ----- + ----- + ----- + 4440
TGGGTCAAACATATGGACGTGACAGGACTGGTAGCGTGTGGCCGAATTGTGATAGTACCTG

a T Q F D T C T V L T I A H R L N T I M D -
TACACCAGGGTCCTGGTCCTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAAC
4441 ----- + ----- + ----- + ----- + ----- + ----- + 4500
ATGTGGTCCCAGGACCAGGACCTGTTTCCTCATCATCGACTTAAACTAAGAGGTGCGGTTG

a Y T R V L V L D K G V V A E F D S P A N -
CTCATTGCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAA
4501 ----- + ----- + ----- + ----- + ----- + ----- + 4557
GAGTAACGTCGATCTCCGTAGAAGATGCCCTACCGGTCTCTACGACCTGAACGGATT

a L I A A R G I F Y G M A R D A G L A * -

Figure 14K

MOAT E cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

ATGGCCGCGCCTGCTGAGCCCTGCGCGGGGCAGGGGGTCTGGAACCAGACAGAGCCTGAA
1 -----+-----+-----+-----+-----+-----+ 60
TACCGGCGCGGACGACTCGGGACGCGCCCCGTCCCCCAGACCTTGGTCTGTCTCGGACTT

a M A A P A E P C A G Q G V W N O T E P E -

CCTGCCGCCACCAGCCTGCTGAGCCTGTGCTTCCTGAGAACAGCAGGGGTCTGGGTACCC
61 -----+-----+-----+-----+-----+-----+ 120
GGACGGCGGTGGTCTGGACGACTCGGACACGAAGGACTCTTGTCGTCCCCAGACCCATGGG

a P A A T S L L S L C F L R T A G V W V P -

CCCATGTACCTCTGGGTCCTTGGTCCCCTACCTCCTCTTCATCCACCACCATGGCCGG
121 -----+-----+-----+-----+-----+-----+ 180
GGGTACATGGAGACCCAGGAACCAGGGTAGATGGAGGAGAAGTAGGTGGTGGTACCGGCC

a P M Y L W V L G P I Y L L F I H H H G R -

GGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTGCCCCTCATA
181 -----+-----+-----+-----+-----+-----+ 240
CCGATGGAGGCCTACAGGGGTGAGAAGTTTCGGTTCTACCACGAACCTAAGCGGGAGTAT

a G Y L R M S P L F K A K M V L G F A L I -

GTCCTGTGTACCTCCAGCGTGGCTGTCGCTCTTTGGAAAATCCAACAGGGAACGCCTGAG
241 -----+-----+-----+-----+-----+-----+ 300
CAGGACACATGGAGGTCGCACCGACAGCGAGAAACCTTTTAGGTTGTCCCTTGC GGACTC

a V L C T S S V A V A L W K I Q Q G T P E -

GCCCCAGAATTCCTCATTCACTACTGTGTGGCTCACCACGATGAGCTTCGCAGTGTTG
301 -----+-----+-----+-----+-----+-----+ 360
CGGGGTCTTAAGGAGTAAGTAGGATGACACACCGAGTGGTGCTACTCGAAGCGTCACAAG

a A P E F L I H P T V W L T T M S F A V F -

CTGATTCACACCGAGAGGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG
361 -----+-----+-----+-----+-----+-----+ 420
GACTAAGTGTGGCTCTCCTTTTCCCTCAGGTCAGTAGACCTCACGACAAACCAATGACC

Figure 15A

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a L I H T E R K K G V Q S S G V L F G Y W .
CTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGCCAGCAGGCCTCCGGAGCGGGCTTC
421 -----+-----+-----+-----+-----+-----+ 480
GAAGAGACGAAACAGAACGGTCGATGGTTGCGACGGGTCGTCCGGAGGCCTCGCCGAAG

a L L C F V L P A T N A A Q Q A S G A G F .
CAGAGCGACCCTGTCCGCCACCTGTCCACCTACCTATGCCTGTCTCTGGTGGTGGCACAG
481 -----+-----+-----+-----+-----+-----+ 540
GTCTCGCTGGGACAGGCGGTGGACAGGTGGATGGATACGGACAGAGACCACCACCGTGTC

a Q S D P V R H L S T Y L C L S L V V A Q .
TTTGTGCTGTCTGCCTGGCGGATCAACCCCCCTTCTCCCTGAAGACCCCAGCAGTCT
541 -----+-----+-----+-----+-----+-----+ 600
AAACACGACAGGACGGACCGCCTAGTTGGGGGGAAGAAGGGACTTCTGGGGGTGTCAGA

a F V L S C L A D Q P P F F P E D P Q Q S .
AACCCCTGTCCAGAGACTGGGGCAGCCTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCT
601 -----+-----+-----+-----+-----+-----+ 660
TTGGGGACAGGTCTCTGACCCCGTCGGAAGGGGAGGTTTCGGTGCAAGACCACCCAAAGA

a N P C P E T G A A F P S K A T F W W V S .
GGCCTGGTCTGGAGGGGATACAGGAGGCCACTGAGACCAAAAGACCTCTGGTCTGCTTGGG
661 -----+-----+-----+-----+-----+-----+ 720
CCGGACCAGACCTCCCCTATGTCCTCCGGTGA CTCTGGTTTTCTGGAGACCAGCGAACCC

a G L V W R G Y R R P L R P K D L W S L G .
AGAGAAAACCTCCTCAGAAGAACTTGTTTCCCGGCTTGAAAAGGAGTGGATGAGGAACCGC
721 -----+-----+-----+-----+-----+-----+ 780
TCTCTTTTGAGGAGTCTTCTTGAACAAAGGGCCGAAC TTTTCTCACCTACTCCTTGGCG

a R E N S S E E L V S R L E K E W M R N R .
AGTGCAGCCCGGAGGCACAACAAGGCAATAGCATTTAAAAGGAAAGGCGGCAGTGGCATG
781 -----+-----+-----+-----+-----+-----+ 840
TCACGTCGGGCCTCCGTGTTGTTCCGTTATCGTAAATTTTCTTTCCGCCGTCACCGTAC

Figure 15B

SUBSTITUTE SHEET (RULE 26)

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a S A A R R H N K A I A F K R K G G S G M .
AAGGCTCCAGAGACCGAGCCCTTCCTACGGCAAGAAGGGAGCCAGTGGCGCCCACTGCTG
841 -----+-----+-----+-----+-----+-----+ 900
TTCCGAGGTCTCTGGCTCGGGAAGGATGCCGTTCTCCCTCGGTCACCGCGGGTGACGAC

a K A P E T E P F L R Q E G S Q W R P L L .
AAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTCCTGGGGACCCTCAGCCTCATCATC
901 -----+-----+-----+-----+-----+-----+ 960
TTCCGGTAGACCGTCCACAAGGTAAGATGGAAGGAGGACCCCTGGGAGTCGGAGTAGTAG

a K A I W Q V F H S T F L L G T L S L I I .
AGTGATGTCTTCAGGTTCACTGTCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGGT
961 -----+-----+-----+-----+-----+-----+ 1020
TCACTACAGAAGTCCAAGTGACAGGGGTTGACGAGTCGGAAAAGGACCTCAAATAACCA

a S D V F R F T V P K L L S L F L E F I G .
GATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCCTCGCCGTGCTGATGTTCTCTCAGCC
1021 -----+-----+-----+-----+-----+-----+ 1080
CTAGGGTTCGGAGGTCGGACCTTCCCATGGAGGAGCGGCACGACTACAAGGAGAGTCGG

a D P K P P A W K G Y L L A V L M F L S A .
TGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAGG
1081 -----+-----+-----+-----+-----+-----+ 1140
ACGGACGTTTGCGACAACTCGTCGTCTTGACATGTCCGAGTTCCACGGCGTCTACTCC

a C L Q T L F E Q Q N M Y R L K V P Q M R .
TTGCGGTTCGGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTCC
1141 -----+-----+-----+-----+-----+-----+ 1200
AACGCCAGCCGGTAGTGACCGGACCACATGTCTTCCAGGACCGAGACAGGTCGCCGAGG

a L R S A I T G L V Y R K V L A L S S G S .
AGAAAGGCCAGTGCGGTGGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCTG
1201 -----+-----+-----+-----+-----+-----+ 1260
TCTTTCGGTTCACGCCACCCACTACACCAGTTAGACCACAGGCACCTGCACGTCGCCGAC

a R K A S A V G D V V N L V S V D V Q R L .

Figure 15C

WO 99/49735

PCT/US99/06644

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ACCGAGAGCGTCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTGC
 1261 -----+-----+-----+-----+-----+-----+ 1320
 TGGCTCTCGCAGGAGATGGAGTTGCCCACACCGACGGAGAGCAGACCTAGCACCCAGACG

a T E S V L Y L N G L W L P L V W I V V C -

TTCGTCTATCTCTGGCAGCTCCTGGGGCCCTCCGCCCTCACTGCCATCGCTGTCTTCCTG
 1321 -----+-----+-----+-----+-----+-----+ 1380
 AAGCAGATAGAGACCGTCGAGGACCCCGGGAGGCGGGAGTGACGGTAGCGACAGAAGGAC

a F V Y L W Q L L G P S A L T A I A V F L -

AGCCTCCTCCCTCTGAATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAGCAA
 1381 -----+-----+-----+-----+-----+-----+ 1440
 TCGGAGGAGGGAGACTTAAAGAAGTAGAGGTTCTTTTCCTTGGTGGTAGTCCTCCTCGTT

a S L L P L N F F I S K K R N H H Q E E Q -

ATGAGGCAGAAGGACTCACGGGCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGACC
 1441 -----+-----+-----+-----+-----+-----+ 1500
 TACTCCGTCTTCCTGAGTGCCCGTGCCGAGTGGTTCGAGATAGGAGTCCTTGAGCTTCTGG

a M R Q K D S R A R L T S S I L R N S K T -

ATCAAGTTCCATGGCTGGGAGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCAG
 1501 -----+-----+-----+-----+-----+-----+ 1560
 TAGTTCAAGGTACCGACCCTCCCTCGGAAAGACCTGTCTCAGGACCCGTAGGCTCCGGTC

a I K F H G W E G A F L D R V L G I R G Q -

GAGCTGGGCGCCTTGCGGACCTCCGGCCTCCTCTTCTGTGTGCTGGTGTCTTCCAA
 1561 -----+-----+-----+-----+-----+-----+ 1620
 CTCGACCCGCGGAACGCCTGGAGGCCGGAGGAGAAGAGACACAGCGACCACAGGAAGGTT

a E L G A L R T S G L L F S V S L V S F Q -

GTGTCTACATTTCTGGTCGCACTGGTGGTGGTTTGTGTGCCACACTCTGGTGGCCGAGAAT
 1621 -----+-----+-----+-----+-----+-----+ 1680
 CACAGATGTAAAGACCAGCGTGACCACCACAAACGACAGGTGTGAGACCACCGGCTCTTA

a V S T F L V A L V V F A V H T L V A E N -

Figure 15D

WO 99/49735

PCT/US99/06644

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GCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAAGGCC
 1681 -----+-----+-----+-----+-----+-----+ 1740
 CGATACTTACGTCTCTTTTCGGAAACACTGAGAGTGTCAAGAGTTGTAGGAGTTGTTCCGG

a A M N A E K A F V T L T V L N I L N K A .

CAGGCTTTCCTGCCCTTCTCCATCCACTCCCTCGTCCAGGCCCGGGTGTCTTTGACCGT
 1741 -----+-----+-----+-----+-----+-----+ 1800
 GTCCGAAAGGACGGGAAGAGGTAGGTGAGGGAGCAGGTCCGGGCCACAGGAAACTGGCA

a Q A F L P F S I H S L V Q A R V S F D R .

CTGGTCACCTTCTCTGCCTGGAAGAAGTTGACCCTGGTGTCTAGACTCAAGTTCCTCT
 1801 -----+-----+-----+-----+-----+-----+ 1860
 GACCAGTGAAGGAGACGGACCTTCTTCAACTGGGACCACAGCATCTGAGTTCAAGGAGA

a L V T F L C L E E V D P G V V D S S S S .

GGAAGCGCTGCCGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTCCCAG
 1861 -----+-----+-----+-----+-----+-----+ 1920
 CCTTCGCGACGGCCCTTCTAACGTAGTGGTATGTGTACGGTGGAAGCGGACCAGGGTC

a G S A A G K D C I T I H S A T F A W S Q .

GAAAGCCCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCTGGCT
 1921 -----+-----+-----+-----+-----+-----+ 1980
 CTTTCGGGAGGGACGGAGGTGTCTTATTTGGAGTGCCACGGGGTCCCGACAGACGACCGA

a E S P P C L H R I N L T V P Q G C L L A .

GTTGTGGTCCAGTGGGGGCAGGGAAGTCTCCCTGCTGTCCGCCCTCTTGGGGAGCTG
 1981 -----+-----+-----+-----+-----+-----+ 2040
 CAACAGCCAGGTACCCCCGTCCCTTCAGGAGGGACGACAGGCGGGAGGAACCCCTCGAC

a V V G P V G A G K S S L L S A L L G E L .

TCAAAGGTGGAGGGGTTCTGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGAGGCC
 2041 -----+-----+-----+-----+-----+-----+ 2100
 AGTTTCCACCTCCCCAAGCACTCGTAGCTCCACGACACCGGATGCACGGGGTCTCCGG

a S K V E G F V S I E G A V A Y V P Q E A .

TGGGTGCAGAACACCTCTGTGGTAGAGAAATGTGTGCTTCGGGCAGGAGCTGGACCCACCC

Figure 15E

SUBSTITUTE SHEET (RULE 26)

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2101 -----+-----+-----+-----+-----+-----+ 2160
ACCCACGTCTTGTGGAGACACCATCTCTTACACACGAAGCCCGTCCTCGACCTGGGTGGG
a W V Q N T S V V E N V C F G Q E L D P P .

TGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCTGAG
2161 -----+-----+-----+-----+-----+-----+ 2220
ACCGACCTCTCTCATGATCTTCGGACACGGGACGTCGGTCTACACCTGTCTGAAGGGACTC
a W L E R V L E A C A L O P D V D S F P E .

GGAATCCACACTTCAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAGCAGCGG
2221 -----+-----+-----+-----+-----+-----+ 2280
CCTTAGGTGTGAAGTTAACCCTCGTCCCGTACTTAGAGAGGCCTCCGGTCTTCGTCGCC
a G I H T S I G E Q G M N L S G G Q K Q R .

CTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCCCTG
2281 -----+-----+-----+-----+-----+-----+ 2340
GACTCGGACCGGGCCCGACATATGTCTTCCGTGACACATGGACGACCTACTGGGGGAC
a L S L A R A V Y R K A A V Y L L D D P L .

GCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGGTGGG
2341 -----+-----+-----+-----+-----+-----+ 2400
CGCCGGGACCTACGGGTGCAACCGGTCGTACAGAAGTTGGTCCAGTAACCCGGACCACCC
a A A L D A H V G Q H V F N Q V I G P G G .

CTACTCCAGGGAACAACACGGATTCTCGTGACGCACGCACTCCACATCCTGCCCCAGGCT
2401 -----+-----+-----+-----+-----+-----+ 2460
GATGAGGTCCCTTGTGTGCCTAAGAGCACTGCGTGCGTGAGGTGTAGGACGGGGTCCGA
a L L Q G T T R I L V T H A L H I L P Q A .

GATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCTACCAGGAGCTT
2461 -----+-----+-----+-----+-----+-----+ 2520
CTAACCTAGTATCACGACCGTTTACCCCGGTAGCGTCTCTACCCAAGGATGGTCCTCGAA
a D W I I V L A N G A I A E M G S Y Q E L .

CTGCAGAGGAAGGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA
2521 -----+-----+-----+-----+-----+-----+ 2580

Figure 15F

GACGTCTCCTTCCCCGGGAGCACACAGAAAGACETAGTTCGGTCTGTCCGGTCCTCTATCT

a L Q R K G A L V C L L D Q A R Q P G D R .

GGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCAGAGGCACCTCTGCAGGC
2581 -----+-----+-----+-----+-----+ 2640
CCTCTTCTCTTTGTCTTGGACCCTGGTCTGGTTCCTGGGGTCTCCGTGGAGACGTCCG

a G E G E T E P G T S T K D P R G T S A G .

AGGAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTCCCTGAGAAGGACCGTACC
2641 -----+-----+-----+-----+-----+ 2700
TCCTCCGGGCTCGAATCTGCGCTCTCCAGGTAGTTCAGTCAGGGACTCTTCTGGCATGG

a R R P E L R R E R S I K S V P E K D R T .

ACTTCAGAAGCCCAGACAGAGGTTCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCA
2701 -----+-----+-----+-----+-----+ 2760
TGAAGTCTTCGGGTCTGTCTCCAAGGAGACCTACTGGGACTGTCCCGTCTACCGGTCTGT

a T S E A Q T E V P L D D P D R A G W P A .

GGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGT
2761 -----+-----+-----+-----+-----+ 2820
CCTTCTCTGTCTAGGTTATGCCGTCCCACTTCCGGTGTACGTGGACCGGATGGACGCA

a G K D S I Q Y G R V K A T V H L A Y L R .

GCCGTGGGCACCCCCCTCTGCCTCTACGCACTCTTCTCTTCTCTGCCAGCAAGTGGCC
2821 -----+-----+-----+-----+-----+ 2880
CGGCACCCGTGGGGGGAGACGGAGATGCGTGAGAAGGAGAAGGAGACGGTCTGTTACCGG

a A V G T P L C L Y A L F L F L C Q Q V A .

TCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGGCGGACGACCCTGCAGTAGGTGGGCAG
2881 -----+-----+-----+-----+-----+ 2940
AGGAAGACGGCCCCGATGACCGACTCGGACACCCGCCTGCTGGGACGTCTCCACCCGTC

a S F C R G Y W L S L W A D D P A V G G Q .

CAGACGCAGGCAGCCCTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATT
2941 -----+-----+-----+-----+-----+ 3000
GTCTGCGTCCGTGCGGACGCACCGCCCTAGAAGCCCGAGGAGCCGACAGAGGTTTCGGTAA

Figure 15G

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a Q T Q A A L R G G I F G L L G C L Q A I .
GGGCTGTTTGCCTCCATGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTC
3001 + + + + + 3060
CCCGACAAACGGAGGTACCGACGCCACGAGGATCCACCCGGGCCCCGTAGGTCCAACGAG

a G L F A S M A A V L L G G A R A S R L L .
TTCCAGAGGCTCCTGTGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCC
3061 + + + + + 3120
AAGGTCTCCGAGGACACCCTACACCACGCTAGAGGGTAGTGAAGAACTCGCCTGTGGG

a F O R L L W D V V R S P I S F F E R T P .
ATTGGTCACCTGCTAAACCGCTTCTCCAAGGAGACAGACACGGTTGACGTGGACATTCCA
3121 + + + + + 3180
TAACCACTGGACGATTTGGCGAAGAGGTTCTCTGTCTGTGCCAACTGCACCTGTAAGGT

a I G H L L N R F S K E T D T V D V D I P .
GACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTG
3181 + + + + + 3240
CTGTTTGAGGCCAGGGACGACTACATGCGGAAACCTGAGGACCTCCAGTCGGACCACCAC

a D K L R S L L M Y A F G L L E V S L V V .
GCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG
3241 + + + + + 3300
CGTCACCGATGGGGTGACCGGTGACACCGGTAGGACGGTGACAAAGAGGAGATGCGACCC

a A V A T P L A T V A I L P L F L L Y A G .
TTTCAGAGCCTGTATGTGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAGCCAGCTAC
3301 + + + + + 3360
AAAGTCTCGGACATACACCAATCGAGTACGGTCGACTCTGCGAACCTCAGTCGGTCGATG

a F Q S L Y V V S S C Q L R R L E S A S Y .
TCGTCTGTCTGCTCCACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTG
3361 + + + + + 3420
AGCAGACAGACGAGGGTGTACCGACTCTGCAAGGTCCCGTCGTGTCAACAGGCCCGTAAG

Figure 15H

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a S S V C S H M A E T F Q G S T V V R A F .
CGAACCCAGGCCCTCTTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATC
3421 -----+-----+-----+-----+-----+ 3480
GCTTGGGTCCGGGGAGAACACCGAGTCTTGTTACGAGCGCATCTACTTTCGGTCTCCTAG

a R T O A P L V A O N N A R V D E S Q R I .
AGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAAT
3481 -----+-----+-----+-----+-----+ 3540
TCAAAGGGCGCTGACCACCGACTGTCCACCGAACGCCGGTTACACCTCGAGGACCCCTTA

a S F P R L V A D R W L A A N V E L L G N .
GGCCTGGTGTTCGAGCTGCCACGTGTGCTGTGCTGAGCAAAGCCACCTCAGTGCTGGC
3541 -----+-----+-----+-----+-----+ 3600
CCGGACCACAAACGTCGACGGTGCACACGACGACTCGTTTCGGGTGGAGTCACGACCG

a G L V F A A A T C A V L S K A H L S A G .
CTCGTGGGCTTCTCTGTCTCTGCTGCCCTCCAGGTGACCCAGGCACTGCAGTGGGTTGTT
3601 -----+-----+-----+-----+-----+ 3660
GAGCACCCGAAGAGACAGAGACGACGGGAGGTCCACTGGGTCCGTGACGTCACCCAACAA

a L V G F S V S A A L Q V T Q A L Q W V V .
CGCAACTGGACAGACCTAGAGAACAGCATCGTGTGAGTGGAGCGGATGCAGGACTATGCC
3661 -----+-----+-----+-----+-----+ 3720
GCGTTGACCTGTCTGGATCTCTTGTCGTAGCACAGTCACCTCGCCTACGTCCTGATACGG

a R N W T D L E N S I V S V E R M Q D Y A .
TGGACGCCCAAGGAGGCTCCCTGGAGGCTGCCACATGTGCAGCTCAGCCCCCTGGCCT
3721 -----+-----+-----+-----+-----+ 3780
ACCTGCGGGTTCCTCCGAGGGACCTCCGACGGGTGTACACGTCGAGTCGGGGGGACCGGA

a W T P K E A P W R L P T C A A Q P P W P .
CAGGGCGGGCAGATCGAGTTCCGGGACTTTGGGCTAAGATACCGACCTGAGCTCCCGCTG
3781 -----+-----+-----+-----+-----+ 3840
GTCCCGCCCGTCTAGCTCAAGGCCCTGAAACCCGATTCTATGGCTGGACTCGAGGGCGAC

a Q G G Q I E F R D F G L R Y R P E L P L .

Figure 15I

GCTGTGCAGGGCGTGTCCCTCAAGATCCACGCAGGAGAGAAGGTGGGCATCGTTGGCAGG
 3841 -----+-----+-----+-----+-----+-----+ 3900
 CGACACGTCCCGCACAGGGAGTTCTAGGTGCGTCTCTCTTCCACCCGTAGCAACCGTCC

a A V Q G V S L K I H A G E K V G I V G R -

ACCGGGGCAGGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAG
 3901 -----+-----+-----+-----+-----+-----+ 3960
 TGGCCCCGTCCCTTCAGGAGGGACCGGTACCCGACGACGCCGAGGTCCTCCGTCGACTC

a T G A G K S S L A S G L L R L Q E A A E -

GGTGGGATCTGGATCGACGGGGTCCCCATTGCCACGTGGGGCTGCACACACTGCGCTCC
 3961 -----+-----+-----+-----+-----+-----+ 4020
 CCACCCTAGACCTAGCTGCCCCAGGGGTAACGGGTGCACCCCGACGTGTGTGACGCGAGG

a G G I W I D G V P I A H V G L H T L R S -

AGGATCAGCATCATCCCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTC
 4021 -----+-----+-----+-----+-----+-----+ 4080
 TCCTAGTCGTAGTAGGGGGTCTGGGGTAGGACAAGGGACCGAGAGACGCCTACTTGGAG

a R I S I I P Q D P I L F P G S L R M N L -

GACCTGCTGCAGGAGCACTCGGACGAGGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTC
 4081 -----+-----+-----+-----+-----+-----+ 4140
 CTGGACGACGTCCTCGTGAGCCTGCTCCGATAGACCCGTCGGGACCTCTGCCACGTCGAG

a D L L Q E H S D E A I W A A L E T V Q L -

AAAGCCTTGGTGGCCAGCCTGCCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAG
 4141 -----+-----+-----+-----+-----+-----+ 4200
 TTTCGGAACCAACCGGTCGGACGGGGCCGGTCGACGTCATGTTACACGACTGGCTCCGCTC

a K A L V A S L P G Q L Q Y K C A D R G E -

GACCTGAGCGTGGGCCAGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACC
 4201 -----+-----+-----+-----+-----+-----+ 4260
 CTGGACTCGCACCCGGTCTTTGTGAGGACACAGACCGTGCACGGGAAGAGGCCTTCTGG

a D L S V G Q K Q L L C I A R A L L R K T -

Figure 15J

CAGATCCTCATCCTGGACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATG
4261 -----+-----+-----+-----+-----+-----+ 4320
GTCTAGGAGTAGGACCTGCTCCGATGACGACGGCACCTGGGACCGTGCTCGACGTCTAC

a Q I L I L D E A T A A V D P G T E L O M -

CAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCTCATTGCCACCGCCTG
4321 -----+-----+-----+-----+-----+-----+ 4380
GTCCGGTACGAGCCCTCGACCAAACGTGTACGTGACACGACGAGTAACGGGTGGCGGAC

a Q A M L G S W F A Q C T V L L I A H R L -

CGTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGC
4381 -----+-----+-----+-----+-----+-----+ 4440
GCGAGGCACTACCTGACACGGGCCCAAGACCAGTACCTGTTCCCCGTCCACCGTCTCTCG

a R S V M D C A R V L V M D K G Q V A E S -

GGCAGCCCGGCCAGCTGCTGGCCCAGAAGGGCCTGTTTTACAGACTGGCCCAGGAGTCA
4441 -----+-----+-----+-----+-----+-----+ 4500
CCGTCGGGCCGGGTGACGACCGGGTCTTCCCGGACAAAATGTCTGACCGGGTCCTCAGT

a G S P A Q L L A Q K G L F Y R L A Q E S -

GGCCTGGTCTGA
4501 -----+----- 4512
CCGGACCAGACT

a G L V * -

Figure 15K